

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 : Search time 5.72664 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416
Sequence: 1 DIQMTQSPASLSASVGRVT.....QPEDFATYTCFGQGTLEIK 79

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	335	80.5	108 1 K1HUU	Ig kappa chain V-I
2	335	80.5	120 2 S4G370	Ig kappa chain V-J
3	334	80.3	123 2 S4G331	Ig kappa chain - h
4	330	79.3	107 2 S3G269	Ig kappa chain V
5	330	79.3	127 2 S4G367	Ig kappa chain V-J
6	330	79.3	129 2 S4G369	Ig kappa chain - h
7	330	79.3	129 2 S52789	Ig kappa chain V
8	327	78.6	108 2 B49047	Ig kappa chain V
9	326	78.4	117 2 S4G371	Ig kappa chain V-J
10	326	78.4	123 2 S4G313	Ig kappa chain V-J
11	324	77.9	125 2 S4G333	Ig kappa chain V-J
12	323.5	77.8	124 2 S4G336	Ig kappa chain V-J
13	323.5	77.5	105 2 A27588	Ig kappa chain V-I
14	322.5	77.5	125 2 S4G315	Ig kappa chain - h
15	322	77.4	108 1 K1HUU	Ig kappa chain V-I
16	322	77.4	108 1 K1HUU	Ig kappa chain V-I
17	322	77.4	108 1 K1HUU	Ig kappa chain V-I
18	322	77.4	108 1 K1HUU	Ig kappa chain V-I
19	322	77.4	108 1 K1HUU	Ig kappa chain V-I
20	320	76.9	108 1 K1HUU	Ig kappa chain V-I
21	320	76.9	108 1 K1HUU	Ig kappa chain V-I
22	320	76.8	107 2 S3G275	Ig kappa chain V-I
23	319.5	76.8	107 2 S3G275	Ig kappa chain V-I
24	318.5	76.6	107 2 S47183	Ig kappa chain - h
25	318	76.4	110 2 K1HUU	Ig kappa chain V-I
26	318	76.4	110 2 S44118	Ig kappa chain V-I
27	318	76.4	125 2 S4G349	Ig kappa chain V-J
28	318	76.4	126 2 S4G335	Ig kappa chain V-J
29	318	76.4	129 1 K1HUU	Ig kappa chain pre

30	318	76.4	129 2 S52793	Ig kappa chain V
31	317	76.2	107 2 U10139	Ig kappa chain V
32	317	76.2	108 1 K1HUU	Ig kappa chain V-I
33	317	76.2	108 1 K1HUU	Ig kappa chain V-I
34	317	76.2	108 1 K1HUU	Ig kappa chain V-I
35	317	76.2	109 2 S31981	Ig kappa chain - h
36	316.5	76.1	106 2 PC2397	Ig kappa chain (BR
37	316	76.0	108 2 I39154	Ig kappa chain (BR
38	315	75.7	107 2 S3G262	Ig kappa chain V-J
39	315	75.7	107 2 S3G262	Ig kappa chain V
40	315	75.7	107 2 S3G262	Ig kappa chain V
41	315	75.7	107 2 S3G262	Ig kappa chain V
42	314	75.5	108 1 K1HUU	Ig kappa chain V-I
43	314	75.5	105 2 S4G316	Ig kappa chain - h
44	313.5	75.4	108 2 S3G521	Ig kappa chain V
45	313	75.2	108 1 K1HUU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

K1HUU
Ig kappa chain V-I region (Hau) - human

C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000

C:Accession: A01668, S02574
R:Marande, S.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970

A:Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg

A:Reference number: A01668; PMID:1032830; PMID:4097974

A:Accession: A01668

A:Molecule type: protein

A:Residues: 1-108 <MAT>

A:Note: The C region of this chain has the Inv (3) marker

R:Steiner, V.; Chang, J.Y

FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the

A:Reference number: S02572; PMID:88005152; PMID:315831

A:Contents: annotation

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F,16-90/Domain: immunoglobulin homology <IMM>

F,23-88/Disulfide bonds: #status predicted

Query Match 80.5%; Score 335; DB 1; Length 108;
Best Local Similarity 67.3%; Pred. No. 4e-26; 2; Indels 28; Gaps 4;
Matches 72; Conservative 5; Mismatches 2;

QY 1 DIQMTQSPASLSASVGRVTTC-----NYLQPKGKRG-LTY-----GYPS 41
DB 1 DIQMTQSPASLSASVGRVTTCRASQISYSLWYQKPKKQVLIYAASSLPSEVPS 60
QY 42 RFSGSGSGTDFTLTSSLPEDFATYTC-----FGQGTLEIK 79
DB 61 RFSGSGSGTDFTLTSSLPEDFATYTCQNVITRTSGQGTLEIK 107

RESULT 2

S4G370
Ig kappa chain V-J region (T3-9) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C:Accession: S4G370; S38644

R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994

A>Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene re
 A:Reference number: S46369; MUID:94313975; PMID:8039491
 A:Accession: S46370
 A:Molecule type: mRNA
 A:Residues: 1-120 <BBN>
 A:Cross-references: EMBL:Z27171; NID:G415957; PIDN:CAA81695.1; PID:G415958
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 335; DB 2; Length 120;
 Best Local Similarity 67.6%; Pred. No. 4.4e-26;
 Matches 73; Conservative 3; Mismatches 2; Indels 30; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTITC-----WYLOKPKSPQ-LIY-----GVPS 41
 Db 11 DIQMTGSPSSLSASVGDRTITCRASRISFLNWTQKPKAPQLIYAVGRLSQGVPS 70
 QY 42 RFGSGSGTDFPFTISSLOPEDFATYYC-----FGQGTKEIK 78
 Db 71 RFGSGSGTDFLTITISSLOPEDFATYYCQGSFNPPEYFGQGTKEIK 118

RESULT 3
 S40331
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40331
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40331
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-123 <KLB>
 A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 334; DB 2; Length 123;
 Best Local Similarity 67.3%; Pred. No. 5.7e-26;
 Matches 72; Conservative 5; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTITC-----WYLOKPKSPQ-LIY-----GVPS 41
 Db 17 DIQMTGSPSSLSASVGDRTITCRASQISISYLNWTQKPKAPKLIYAAASLSQGVPS 76
 QY 42 RFGSGSGTDFPFTISSLOPEDFATYYC-----FGQGTKEIK 79
 Db 77 RFGSGSGTDFLTITISSLOPEDFATYYCQGSYTPPTFGQGTKEIK 123

RESULT 4
 S36269
 Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C:Accession: S36269
 R:Giffiths, A.D.; Malmqvist, M.; Marks, U.D.; Bye, U.M.; Embleton, M.J.; McCafferty, J.
 EMBL J. 12, 725-734, 1993
 A>Title: Human anti-self antibodies with high specificity from phage display libraries.
 A:Reference number: S36256; MUID:93178448; PMID:7679950
 A:Accession: S36269
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <GRI>
 A:Cross-references: EMBL:Z18838; NID:G33422; PIDN:CAA79290.1; PID:G939915
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 107;
 Best Local Similarity 67.3%; Pred. No. 1.2e-25;
 Matches 72; Conservative 4; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTITC-----WYLOKPKSPQ-LIY-----GVPS 41
 Db 1 DIQMTGSPSSLSASVGDRTITCRASQIRNDLWYQKPKAPKLIYGTSSLSQGVPS 60
 QY 42 RFGSGSGTDFPFTISSLOPEDFATYYC-----FGQGTKEIK 79
 Db 61 RFGSGSGTDFLTITISSLOPEDFATYYCQGSYTPPTFGQGTKEIK 107

RESULT 5
 S40367
 Ig kappa chain V-J-C region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40367
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40367
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-127 <KLB>
 A:Cross-references: EMBL:X72477
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 127;
 Best Local Similarity 66.4%; Pred. No. 1.4e-25;
 Matches 71; Conservative 6; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTITC-----WYLOKPKSPQ-LIY-----GVPS 41
 Db 18 DIQMTGSPSSLSASVGDRTITCRASQISISYLNWTQKPKAPKLIYAAASLSQGVPS 77
 QY 42 RFGSGSGTDFPFTISSLOPEDFATYYC-----FGQGTKEIK 79
 Db 78 RFGSGSGTDFLTITISSLOPEDFATYYCQGSYTPPTFGQGTKEIK 124

RESULT 6
 S40369
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40369
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40369
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <KLB>
 A:Cross-references: EMBL:X72479; NID:G441426; PIDN:CAA51147.1; PID:G441427
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 129;
 Best Local Similarity 66.4%; Pred. No. 1.5e-25;
 Matches 71; Conservative 6; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQMTGSPASLSASVGDRTITC-----WYLOKPKSPQ-LIY-----GVPS 41
 Db 22 DIQMTGSPSSLSASVGDRTITCRASVITSNHLYWFOQKPKAPKLIYAAASLSQGVPS 81


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QY 42 RFSGSGGTDFPTTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 82 KFSGSGGTDFLTITSSLPQEDFATYYCQVNSYPTTFGQGTKLEIK 128

RESULT 7
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52789
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A:Reference number: S52789
A:Accession: S52789
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85995; NID:G758588; PIDN:CAA59987.1; PID:G758589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 330; DB 2; Length 129;
Best Local Similarity 65.4%; Pred. No. 1.5e-25;
Matches 70; Conservative 5; Mismatches 4; Indels 28; Gaps 3;

QY 1 DIQWTSPLASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPS 41
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 DIQWTSPLSLSASVGDRTVITCQASQDISNLYNWYQKPKAPKLLIHAASLSLETGVPS 82

QY 42 RFSGSGGTDFPTTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 RFSGSGGTDFPTTISLQPEDFATYYCQVNSYPTTFGQGTKLEIK 129

RESULT 8
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Experimental source: thymic B lymphocytes
A>Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 327; DB 2; Length 108;
Best Local Similarity 66.4%; Pred. No. 2.4e-25;
Matches 71; Conservative 5; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQWTSPLASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPS 41
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQWTSPLSLSASVGDRTVITCRASQSSISNLYNWYQKPKAPKLLIYAASLSQSGVPS 60

QY 42 RFSGSGGTDFPTTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RFSGSGGTDFLTITSSLPQEDFATYYCQVNSYPTTFGQGTKLEIK 107

RESULT 9
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
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C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R:Bensimon, C.; Chaetagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z27172; NID:G415959; PIDN:CAA81596.1; PID:G415960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 326; DB 2; Length 117;
Best Local Similarity 64.2%; Pred. No. 3.3e-25;
Matches 70; Conservative 7; Mismatches 2; Indels 30; Gaps 4;

QY 1 DIQWTSPLASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPS 41
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 DIQWTSPLSLSASVGDRTVITCRASRSISTWLAWYQKPKAPKLLIYKASTLESQVPS 67

QY 42 RFSGSGGTDFPTTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 RFSGSGGTDFLTITSSLPQEDFATYYCQVNSYPTTFGQGTKLEIK 116

RESULT 10
S40313
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40313
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40313
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72423; NID:G441314; PIDN:CAA51091.1; PID:G441315
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 78.4%; Score 326; DB 2; Length 123;
Best Local Similarity 65.4%; Pred. No. 3.5e-25;
Matches 70; Conservative 7; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQWTSPLASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPS 41
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 DIQWTSPLSLSASVGDRTVITCRASQIRNDLAWFOQKPKAPKRLIYDAASLLSGVPS 76

QY 42 RFSGSGGTDFPTTISLQPEDFATYYC-----FGQGTKLEIK 79
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 RFSGSGGTDFLTITSSLPQEDFATYYCQVNSYPTTFGQGTKLEIK 123

RESULT 11
S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40333
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
```

A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 324; DB 2; Length 125;
Best Local Similarity 64.5%; Pred. No. 5.5e-25;
Matches 69; Conservative 8; Mismatches 2; Indels 28; Gaps 4;

QY 1 DIQWTSPLASVSGDRVTITC-----WYLPKPKSPQ-LIY-----GVPS 41
DB 19 DIQWTSPLASVSGDRVTITCRASQISSMLAWYQKPKAPKLLIYKASLSGVPS 78
QY 42 RFGSGSGTDFSTISLQPEDFATYTC-----FQGTKEIK 79
DB 79 RFGSGSGTEFTTISLQDDFATYCCQYNSYPWTFQGTKEIK 125

RESULT 12

S40336
IG kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40336
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-124 <KLE>
A;Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 323.5; DB 2; Length 124;
Best Local Similarity 64.8%; Pred. No. 6.1e-25;
Matches 70; Conservative 6; Mismatches 3; Indels 29; Gaps 4;

QY 1 DIQWTSPLASVSGDRVTITC-----WYLPKPKSPQ-LIY-----GVPS 41
DB 16 DIQWTSPLASVSGDRVTITCRASQISSMLAWYQKPKAPKLLIYKASLSGVPS 75
QY 42 RFGSGSGTDFSTISLQPEDFATYTC-----FQGTKEIK 79
DB 76 RFGSGSGTEFTTISLQDDFATYCCQYNSYPWTFQGTKEIK 123

RESULT 13

IG kappa chain V-I region (Wil[2]) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: A27585
R;Goni, F.; Chuba, J.; Buxbaum, J.; Frangione, B.
J. Immunol. 140, 551-557, 1988
A;Title: A double monoclonal IgG1-kappa and IgG2-kappa in a single myeloma patient. Vari
A;Reference number: A28280; MUID:86088671; PMID:3121749
A;Accession: A27585
A;Molecule type: protein
A;Residues: 1-105 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 322.5; DB 2; Length 105;
Best Local Similarity 66.3%; Pred. No. 6.5e-25;
Matches 69; Conservative 7; Mismatches 3; Indels 25; Gaps 4;

QY 1 DIQWTSPLASVSGDRVTITC-----WYLPKPKSPQ-LIY-----GVPS 41
DB 19 DIQWTSPLASVSGDRVTITCRASQISSMLAWYQKPKAPKLLIYKASLSGVPS 78
QY 42 RFGSGSGTDFSTISLQPEDFATYTC-----FQGTKEIK 79
DB 79 RFGSGSGTEFTTISLQDDFATYCCQYNSYPWTFQGTKEIK 125

DB 1 DIQWTSPLASVSGDRVTITCRASQISSMLAWYQKPKAPKLLIYKASLSGVPS 60
QY 42 RFGSGSGTDFSTISLQPEDFATYTC-----FQGTKEIK 79
DB 61 RFGSGSGTEFTTISLQDDFATYCCQYNSYPWTFQGTKEIK 104

RESULT 14

S40315
IG kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40315
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40315
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72425; NID:g441318; PIDN:CAA51093.1; PID:g441319
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 322.5; DB 2; Length 125;
Best Local Similarity 62.0%; Pred. No. 7.8e-25;
Matches 67; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

QY 1 DIQWTSPLASVSGDRVTITC-----WYLPKPKSPQ-LIY-----GVPS 41
DB 16 DIQWTSPLASVSGDRVTITCRASQISSMLAWYQKPKAPKLLIYKASLSGVPS 75
QY 42 RFGSGSGTDFSTISLQPEDFATYTC-----FQGTKEIK 79
DB 76 RFGSGSGTEFTTISLQDDFATYCCQYNSYPWTFQGTKEIK 123

RESULT 15

KHULY
IG kappa chain V-I region (Lay) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 21-Jan-2000
C;Accession: A01871; F30609
R;Capra, J.D.; Klapper, D.G.
Scand. J. Immunol. 5, 677-684, 1976
A;Title: Complete amino acid sequence of the variable domains of two human IgM anti-gam
A;Reference number: A01871; MUID:77038198; PMID:824717
A;Accession: A01871
A;Molecule type: protein
A;Residues: 1-108 <CAP>
A;Note: the second and third hypervariable regions of this chain are identical with tho
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autocat
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: F30609
A;Molecule type: protein
A;Residues: 1-104 <GON>
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status Predicted

Query Match 77.4%; Score 322; DB 1; Length 108;

Best Local Similarity 64.5%; Pred. No. 7.5e-25;
Matches 69; Conservative 6; Mismatches 4; Indels 28; Gaps 4;

Qy 1 DIQWTCSPASISASVGRVTITC-----WYLOKPGKSPQ-LIY-----GVPS 41

Db 1 DIQWTCSPESLSVSVGRVTITCQASQNNVAYLNWYQQKPOLAPKLLIYGASTREAGVPS 60

Qy 42 RFGSGSGTDFSTISSLPEDFATYYC-----FGQTKLEIK 79

Db 61 RFGSGSGTDFSTISSLPEDIATYYCQYNNWPPTFGQTKVEVK 107

Search completed: January 13, 2004, 12:44:39
Job time : 5.72664 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 3.44978 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMTQSPASLSASVGRVT.....QPEDFATYCFGQGTKEIK 79

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335	80.5	108	1	KV1H HUMAN
2	322	77.4	108	1	KV1G HUMAN
3	322	77.4	108	1	KV1M HUMAN
4	322	77.4	108	1	KV1O HUMAN
5	320	76.9	108	1	KV1A HUMAN
6	320	76.9	108	1	KV1R HUMAN
7	318	76.4	108	1	KV1B HUMAN
8	318	76.4	129	1	KV1W HUMAN
9	317	76.2	108	1	KV1C HUMAN
10	317	76.2	108	1	KV1F HUMAN
11	317	76.2	108	1	KV1P HUMAN
12	314	75.5	108	1	KV1K HUMAN
13	313	75.2	108	1	KV1V HUMAN
14	313	75.2	108	1	KV1Y HUMAN
15	312	75.0	108	1	KV1A HUMAN
16	309.5	74.4	107	1	KV1D HUMAN
17	306	73.6	129	1	KV1X HUMAN
18	304	73.1	108	1	KV1Q HUMAN
19	302	72.6	108	1	KV1E HUMAN
20	302	72.6	108	1	KV1L HUMAN
21	299	71.9	108	1	KV1S HUMAN
22	295.5	71.0	109	1	KV1T HUMAN
23	292.5	70.3	117	1	KV1I HUMAN
24	292	70.2	108	1	KV5D MOUSE
25	290.5	69.8	117	1	KV1J HUMAN
26	277	66.6	108	1	KV5J MOUSE
27	274	65.9	112	1	KV1U HUMAN
28	273	65.6	108	1	KV5O MOUSE
29	272	65.4	128	1	KV5E MOUSE
30	272	65.4	149	1	KV5A MOUSE
31	271	65.1	108	1	KV5M MOUSE
32	271	65.1	114	1	KV4A HUMAN
33	270	64.9	108	1	KV5Q MOUSE

34	270	64.9	108	1	KV5S MOUSE
35	270	64.9	108	1	KV5T MOUSE
36	269.5	64.8	115	1	KV5C MOUSE
37	269	64.7	108	1	KV5P MOUSE
38	268.5	64.5	109	1	KV3E HUMAN
39	268.5	64.5	109	1	KV3G HUMAN
40	268.5	64.5	129	1	KV3L HUMAN
41	268	64.4	108	1	KV5K MOUSE
42	268	64.4	108	1	KV5L MOUSE
43	268	64.4	108	1	KV5N MOUSE
44	268	64.4	134	1	KV4C HUMAN
45	266.5	64.1	109	1	KV3D HUMAN

ALIGNMENTS

RESULT 1
KV1H HUMAN
ID KV1H HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE.
RX MEDLINE:71032830; PubMed:4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; KIHUHU.
DR HSSP; P80382; 1WT.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 35 49
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 50 56
FT COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 57 88
FT DISULFID 89 97
FT NON TER 98 107
FT BY SIMILARITY.
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 80.5%; Score 335; DB 1; Length 108;

Best Local Similarity 67.3%; Pred. No. 4.6e-31;

Matches 72; Conservative 5; Mismatches 2; Indels 28; Gaps 4;

Qy 1 DIQMTQSPASLSASVGRVTITICRASSQSISYLSWYQKPKGAPQLIYAASLPSGVPS 60

Db 1 DIQMTQSPASLSASVGRVTITICRASSQSISYLSWYQKPKGAPQLIYAASLPSGVPS 60

Qy 42 RFSGSGSGTDFTLTITSLQPEDFATYCFGQGTKEIK 79

Db 61 RFSGSGSGTDFTLTITSLQPEDFATYCFGQGTKEIK 107

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RN SEQUENCE.
RP MEDLINE=77038198; PubMed=824717;
RX Capra J.D., Klapper D.G.;
RA "Complete amino acid sequence of the variable domains of two human
RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
RL specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11934 MW; 73993A95431434A CRC64;

Query Match 77.4%; Score 322; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.4e-29;
Matches 69; Conservative 6; Mismatches 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASISASVGRVTITC-----WYLOKPKGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSLSVSVDGRVTITCQSQNVAYLNWYQKPKGLAPKLIYGASTREAGVPS 60
QY 42 RFGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFSTTISLQPEDFATYYCQQVNNWPPTEFGQGTKVEIK 107

RESULT 4
KVIM HUMAN
ID KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=70201507; PubMed=5447531;
RX Kohler H., Shimizu A., Paul C., Putnam F.W.;
RA "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59 (1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHOUU.
DR HSSP; P01607; IREI.

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RESULT 2
KVIG HUMAN
ID KVIG HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Gal.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=75059122; PubMed=4215718;
RX Laure C.J., Watanabe S., Hilschmann N.;
RA "The primary structure of a monoclonal IGM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 77.4%; Score 322; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.4e-29;
Matches 69; Conservative 7; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASISASVGRVTITC-----WYLOKPKGKSP-OLIV-----GVPS 41
DB 1 DIQMTQSPSLSVSVDGRVTITCRASQIRNDLTWYQKPKGKAPKELIYVAASNLQSGVPS 60
QY 42 RFGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFSTTISLQPEDFATYYCQVNSVPSRFGQGTKVEIK 107

RESULT 3
KVIM HUMAN
ID KVIM HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DOMAIN 99 108
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT TURN 19 25
 FT TURN 30 31
 FT TURN 33 38
 FT TURN 40 41
 FT TURN 44 49
 FT TURN 50 52
 FT TURN 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT TURN 62 67
 FT TURN 68 69
 FT TURN 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;
 Query Match 77.4%; Score 322; DB 1; Length 108;
 Best Local Similarity 59.8%; Pred. No. 1.4e-29;
 Matches 64; Conservative 13; Mismatches 2; Indels 28; Gaps 4;
 QY 1 DIQMTQSPASLSASVGRVTITC-----WYLQKPKSQ-LIY-----GVPS 41
 DB 1 DIQMTSPSSLSASVGRVTITCRASZTISLWYZZKPKAPBLIYASBLHSGVPS 60
 QY 42 RFGSGSGTDFSTISSLPQEDFYTC-----FGQGTLEIK 79
 DB 61 RFGSGSGTDFSTISSLPZBFATYCYZSSYSTPTFGZGTRLZIK 107
 RESULT 5
 KV10_HUMAN
 ID KV10_HUMAN STANDARD; PRT; 108 AA.
 AC P01607;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-I region Rei.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE.
 RX MEDLINE=76023758; PubMed=8093229;
 RA Palm W., Hilschmann N.;
 RT "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 RN [2]
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE=76039968; PubMed=1182131;
 RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
 RT "The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
 RL Biochemistry 14:4943-4952(1975).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A91663; K1HURE.
 DR PDB; 1REI; 17-FEB-84.
 DR PDB; 1AR2; 12-NOV-97.
 DR PDB; 1BW7; 29-DEC-99.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT STRAND 4 7
 FT STRAND 10 13
 FT TURN 15 16
 FT TURN 19 25
 FT TURN 30 31
 FT TURN 33 38
 FT TURN 40 41
 FT TURN 44 49
 FT TURN 50 52
 FT TURN 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT TURN 62 67
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 FT TURN 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;
 Query Match 76.9%; Score 320; DB 1; Length 108;
 Best Local Similarity 65.1%; Pred. No. 2.3e-29;
 Matches 69; Conservative 6; Mismatches 3; Indels 28; Gaps 4;
 QY 1 DIQMTQSPASLSASVGRVTITC-----WYLQKPKSQ-LIY-----GVPS 41
 DB 1 DIQMTSPSSLSASVGRVTITCRASQDIILYNWYQTPGKAPKLLIYEASNLQGVPS 60
 QY 42 RFGSGSGTDFSTISSLPQEDFYTC-----FGQGTLEIK 78
 DB 61 RFGSGSGTDFSTISSLPQEDFYTCQYQSLPYTFGQGTLEIK 106
 RESULT 6
 KV1R_HUMAN
 ID KV1R_HUMAN STANDARD; PRT; 108 AA.
 AC P01610;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region WEA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83273707; PubMed=6410398;
 RA Goni F., Frangione B.;
 RT "Amino acid sequence of the Fv region of a human monoclonal IGM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
 RT Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
 RL CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH

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CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHUW.
DR HSP; P80362; IWL.
DR GO; 0005576; C:extracellular; NAS.
DR GO; 0003823; F:antigen binding activity; NAS.
DR GO; 0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249561F0945618C CRC64;

Query Match 76.9%; Score 320; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 2.3e-29;
Matches 68; Conservative 8; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKSP-QLIY-----GVPS 41
DB 1 DIQMTQSPSSLSASVGRVITTCASQGIKNDLTWQKQKGTAPKELIYGATSLQSGVPS 60
QY 42 RFGSGSGTDFPSFTISSLPQEDFATYTC-----FQGTKLKLEIK 79
DB 61 RFGSGSGTFTLTNSLPQEDFATYTCLOYSFPPTWTFQGTKEVYK 107

RESULT 7
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlfammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigmann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A91653; KIHUW.
DR PDB; 1JVS; 30-JAN-02.
DR GO; 0005576; C:extracellular; NAS.

GO; 0003823; F:antigen binding activity; NAS.
GO; 0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IG; 1.
PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; B8011187EE6F6B9 CRC64;

Query Match 76.4%; Score 318; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 3.9e-29;
Matches 69; Conservative 5; Mismatches 5; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVITTC-----WYLPKPKSP-QLIY-----GVPS 41
DB 1 DIQMTQSPSSLSASVGRVITTCASQDISDYLNWYQKQKAPKLIYDASNLESVPS 60
QY 42 RFGSGSGTDFPSFTISSLPQEDFATYTC-----FQGTKLKLEIK 79
DB 61 RFGSGSGAHTFTFTISSLPQEDFATYTCQYDYLPWTFQGTKEVYK 107

RESULT 8
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01893; KIHUW.
DR HSP; P01607; IREI.
DR GO; 0005576; C:extracellular; NAS.
DR GO; 0003823; F:antigen binding activity; NAS.
DR GO; 0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IG; 1.
PROSITE; PS0835; IG_LIKE; 1.
```



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KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 FRAMEWORK-3.
FT DOMAIN 72 78 FRAMEWORK-4.
FT DOMAIN 79 110 BY SIMILARITY.
FT DOMAIN 111 129 FRAMEWORK-1.
FT DOMAIN 120 129 FRAMEWORK-2.
FT DOMAIN 120 129 FRAMEWORK-3.
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match 76.4%; Score 318; DB 1; Length 129;
Best Local Similarity 65.4%; Pred. No. 4.7e-29;
Matches 70; Conservative 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41
DB 23 DIQMTQSPSSUSASVGDRTVITCRASQISNLYNWYQKPGKAPKFLIYAASSLQSGVTS 82
QY 42 RFGSGSGTDFSTISSLPQDFATYYC-----FGQGTKLEIK 79
DB 83 RFGSGSGTDFLTLSISLPQDFATYYCQSYSTLTITFGQGTKLEIK 129

RESULT 9
KV1C HUMAN
ID KV1C HUMAN STANDARD; PRT; 108 AA.
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT "Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin b-chain (Bence Jones protein
RT Bi). 3. The complete amino acid sequence and the genetic
RT significance of the variability principles for the mechanism of
RT antibody formation."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01863; KIHUBI.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS003596; IG_V.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 25 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 FRAMEWORK-3.
FT DOMAIN 72 78 FRAMEWORK-4.
FT DOMAIN 79 110 BY SIMILARITY.
FT DOMAIN 111 129 FRAMEWORK-1.
FT DOMAIN 120 129 FRAMEWORK-2.
FT DOMAIN 120 129 FRAMEWORK-3.
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match 76.4%; Score 317; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 5e-29;
Matches 69; Conservative 5; Mismatches 5; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSPFLSASVGDSTVITCQASQIRNSLIWYQKPGKAPKFLIYDAENLSIGVPS 60
QY 42 RFGSGSGTDFSTISSLPQDFATYYC-----FGQGTKLEIK 79
DB 61 RFGSGSGTDFLTSISLPQDFATYYCQSYNLPYTFQGTQKLEIK 107

RESULT 10
KV1F HUMAN
ID KV1F HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A90562; KIHUEU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS003596; IG_LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88923 CRC64;

Query Match 76.2%; Score 317; DB 1; Length 108;
Best Local Similarity 60.7%; Pred. No. 5e-29;
Matches 65; Conservative 10; Mismatches 28; Gaps 3;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSTLSASVGDRTVITCRASQISNTWLAWYQKPGKAPKFLIYKASLESIGVPS 60

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QY 42 RFGSGSGTDFSTTSSLPQDFATYYC-----FGQGTKEIK 79
DB 61 RFTGSGGTFTTSSLPQDFATYYCQYNSDKMFGGTKEVVK 107

RESULT 11
KV1P_HUMAN STANDARD; PRT; 108 AA.
ID KV1P_HUMAN
AC P01608;
DE 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Fraeek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A91638; KIHURY.
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 76.2%; Score 317; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 5e-29;
Matches 68; Conservative 7; Mismatches 4; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPFSLSSASVGRVTITCQASQDISIFLNWYQKPKGKAPKLLIYDASKLEAGVPS 60

QY 42 RFGSGSGTDFSTTSSLPQDFATYYC-----FGQGTKEIK 79
DB 61 RFTGSGGTFTTSSLPQDFATYYCQYNSDKMFGGTKEVVK 107

RESULT 12
KV1K_HUMAN STANDARD; PRT; 108 AA.
ID KV1K_HUMAN
AC P04430;
DE 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RA "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
RL PIR; A01878; KIHUEN.
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AC P01603;
DE 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Ka.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA Shinoda T.;
RT "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL J. Biochem. 77:1277-1296(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01869; KIHUKA.
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding activity; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FBED5A2F4B CRC64;

Query Match 75.5%; Score 314; DB 1; Length 108;
Best Local Similarity 58.9%; Pred. No. 1.1e-28;
Matches 63; Conservative 13; Mismatches 3; Indels 28; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKGKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPFSLSSASVGRVTITCQASQIVLSYLNWYQKPKGKAPKLLIYASLSLETGVPS 60

QY 42 RFGSGSGTDFSTTSSLPQDFATYYC-----FGQGTKEIK 79
DB 61 RFTGSGGTFTTSSLPQDFATYYCQYNSDKMFGGTKEVVK 107

RESULT 13
KVIV_HUMAN STANDARD; PRT; 108 AA.
ID KVIV_HUMAN
AC P04430;
DE 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RA "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
RL PIR; A01878; KIHUEN.
```

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DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 75.2%; Score 313; DB 1; Length 108;
Best Local Similarity 62.6%; Pred. No. 1.4e-28;
Matches 67; Conservative 8; Mismatches 4; Indels 28; Gaps 4;

Qy 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIQMTQSPSSLSASVGRVITTCRASQVYVAVFQKPKAPKSLIYDASTLQSGVPS 60

Qy 42 RFGSGSGTDFSTFISSLPQEDPATIYC-----FGQGTKLEIK 79
Db 61 NFGSGSGTDFILFISSLPQEDPATIYCCQVNSPYFTFGQGTKVQIK 107

RESULT 14
KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
```

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DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 75.2%; Score 313; DB 1; Length 108;
Best Local Similarity 62.6%; Pred. No. 1.4e-28;
Matches 67; Conservative 9; Mismatches 3; Indels 28; Gaps 4;

Qy 1 DIQMTQSPASLSASVGRVITTC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIQMTQSPSSLSASVGRVITTCRASQDITVNVVWFQRPQAPKVIYASILETGVP 60

Qy 42 RFGSGSGTDFSTFISSLPQEDPATIYC-----FGQGTKLEIK 79
Db 61 RFGSGSGTDFSTFISSLPQEDPATIYCCQYDTLPLTFGGGTRVDIK 107

RESULT 15
KVIA_HUMAN STANDARD; PRT; 108 AA.
ID KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
```

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 75.0%; Score 312; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.8e-28;
Matches 69; Conservative 4; Mismatches 6; Indels 28; Gaps 4;

Qy 1 DIQWTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPS 41
Db 1 DIQWTQSPSSLSASVGDRTVITCQASQDINHLYLNWYQGGPKAPKILIIYDASNLETGVPS 60

Qy 42 RFGSGSGTDFSTTISLQPEDPATYYC-----FQGTKEIK 79
Db 61 RFGSGGFGTDFTTISGLQPEDATYYCQOYDTLPRTFGQGTKEIK 107
```

Search completed: January 13, 2004, 12:39:25
Job time : 4.44978 secs

Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQQKPKAPNLLIYAASSLSQGVPS 60
Qy 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCQSYSTSTWTFGGTKVETK 107

RESULT 2
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.B., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577E16 CRC64;

Query Match 78.7%; Score 327.5; DB 4; Length 107;
Best Local Similarity 67.0%; Pred. No. 2.4e-31;
Matches 71; Conservative 5; Mismatches 3; Indels 27; Gaps 4;

Qy 1 DIQMTQSPASLSASVGDRTVITTC-----WYLOKPKGKSPQ-LIY-----GVPS 41
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQQKPKAPNLLIYAASSLSQGVPS 60

Qy 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCQSYSTLTFTGGTKVETK 106

RESULT 3
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

DR EMBL; AF035044; AAD56280.1; -
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.2%; Score 321; DB 4; Length 108;
Best Local Similarity 66.4%; Pred. No. 1.5e-30;
Matches 71; Conservative 3; Mismatches 5; Indels 28; Gaps 4;

Qy 1 DIQMTQSPASLSASVGDRTVITTC-----WYLOKPKGKSPQ-LIY-----GVPS 41
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQQKPKAPNLLIYAASSLSQGVPS 60

Qy 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
Db 61 RFSGSGSGTDFTLTISSLPQEDVATYYCQKNSAPRTFGPGTKLEIK 107

RESULT 4
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035033; AAD56269.1; -
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 070549FDE0754748 CRC64;

Query Match 74.4%; Score 309.5; DB 4; Length 107;
Best Local Similarity 63.2%; Pred. No. 3.4e-29;
Matches 67; Conservative 6; Mismatches 6; Indels 27; Gaps 4;

Qy 1 DIQMTQSPASLSASVGDRTVITTC-----WYLOKPKGKSPQ-LIY-----GVPS 41
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQQKPKAPNLLIYAASSLSQGVPS 60

Qy 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
Db 61 RFSGSGSGTDFTLTISSLPQEDFATYYCQSYSAITFGPGTKVDIR 106

RESULT 5
Q9UL79

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ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IRII.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR NON_TER 1
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 72.4%; Score 301; DB 4; Length 108;
Best Local Similarity 61.7%; Pred. No. 3.6e-28;
Matches 66; Conservative 6; Mismatches 7; Indels 28; Gaps 4;

Qy 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIVMTQSPSLASASGDRVTISCRMSQGISSYLAQYQKPKAPPELLIYASTLSQGVPS 60

Qy 42 RPSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKLEIK 79
Db 61 RPSGSGSGTDFLTITISCLQSEDFATYYCQYYSPPTFGQTKVEIK 107

Query Match 70.4%; Score 293; DB 11; Length 234;
Best Local Similarity 59.8%; Pred. No. 8.3e-27;
Matches 64; Conservative 5; Mismatches 10; Indels 28; Gaps 3;

Qy 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 21 DIQMTQSPASLSASVGTITICRASENIYSYLAQYQKQKSPQLLVYNKTLADGVPS 80

Qy 42 RPSGSGSGTDFSTISSLOPEDFATYYC-----FGQGTKLEIK 79
Db 81 RPSGSRSGTQFSLKINSLOPEDFGSYQCQHHSGIPPTFGSGTKLEIK 127

RESULT 8
Q9QYF0 PRELIMINARY; PRT; 298 AA.
ID Q9QYF0
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CN 8 scFv.
DE CN 8.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phase display subtraction
```



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RT method.":
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
DR ENBL; AB036341; BAA8633.1; -.
DR HSPF; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;

Query Match 70.4%; Score 293; DB 11; Length 298;
Best Local Similarity 58.9%; Pred. No. 1.1e-26;
Matches 63; Conservative 7; Mismatches 9; Indels 28; Gaps 3;

QY 1 DIQWTQSPASLSASVGDRTVITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 173 DIETQSPASLSASVGETVITTCRAGNHNLYAWYQKQKSPQLVYNKTLADGVPS 232
QY 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 233 RFSGSGSGTQSLKINSLPQEDFGSYVCQHFMTPTVTFGGTKLEIK 279

RESULT 9
Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa 1 light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden."
RL Blood 98:714-720 (2001).
DR ENBL; AF361758; AAK51465.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 69.0%; Score 287; DB 4; Length 116;
Best Local Similarity 57.9%; Pred. No. 1.8e-26;
Matches 62; Conservative 9; Mismatches 8; Indels 28; Gaps 4;

QY 1 DIQWTQSPASLSASVGDRTVITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 1 DIQWTQSPSSLSASVGRVTITCQASQDIANHLNWKYKPGKFLIYDGSFLTKGVPS 60
QY 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 61 RFSGSGSATNFTVITSSLPQEDFATYYCQVHHLPTFTFGPTKVDFK 107

RESULT 10
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819 (1997).
DR ENBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 67.4%; Score 280.5; DB 11; Length 241;
Best Local Similarity 55.7%; Pred. No. 2.6e-25;
Matches 59; Conservative 12; Mismatches 8; Indels 27; Gaps 4;

QY 1 DIQWTQSPASLSASVGRVTITC-----WYLOKPGKSPQLIY-----GVPS 41
DB 134 DIETQSPSSLSASLGKGVITTCASQDINKYIANYOHKPGKSPSHTLIYIQGPIS 193
QY 42 RFSGSGSGTDFSTISSLPQEDFATYYC-----FGQGTKLEIK 79
DB 194 RFSGSGSGRDYFSISNLEPDIATYCYLHYDNLHTFGGTKLEIK 239

RESULT 11
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 25.8 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS0290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 233
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 67.3%; Score 280; DB 11; Length 233;
Best Local Similarity 58.9%; Pred. No. 2.9e-25;
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Matches 63; Conservative 7; Mismatches 9; Indels 28; Gaps 4;
QY 1 DIQMTQSPASISASVGDRTVITC-----WYLOKP-GKSPQLIY-----GVPS 41
DB 20 DIQMTQTSSLSASLGDRTVITCSGSGQSIANYLNWYQKPDGTGTVKLLIYTTSSLHSGVPS 79
QY 42 RPSGSGSGTDFSTTSSLPQDFATYYC-----FGQGTGLEIK 79
DB 80 RPSGSGSGTDFSTTSSLPQDFATYYCQYRYLPWFPGGKLEIK 126

RESULT 12
Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scfv)".
RL Submitted (MAY-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 66.8%; Score 278; DB 11; Length 214;
Best Local Similarity 57.0%; Pred. No. 4.5e-25;
Matches 61; Conservative 9; Mismatches 9; Indels 28; Gaps 4;
QY 1 DIQMTQSPASISASVGDRTVITC-----WYLOKPQKSPQ-LIY-----GVPS 41
DB 1 DIQMTQSPSYASLGERVITTCASQDINSYLSWFOQPKSPKPTLIYRANRLVDGVP 60
QY 42 RPSGSGSGTDFSTTSSLPQDFATYYC-----FGQGTGLEIK 79
DB 61 RPSGSGSQDYSLTISLSEYEDMGIIYCLQYDEFFTFGSGKLEIK 107

RESULT 13
Q9R062 PRELIMINARY; PRT; 234 AA.
AC Q9R062;
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
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DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 66.1%; Score 275; DB 11; Length 234;
Best Local Similarity 57.9%; Pred. No. 1.2e-24;
Matches 62; Conservative 7; Mismatches 10; Indels 28; Gaps 4;
QY 1 DIQMTQSPASISASVGDRTVITC-----WYLOKP-GKSPQLIY-----GVPS 41
DB 21 DIQMTQTSSLSASLGDRTVITCSASQGISNLYNLYQKPDGTGTVKLLIYTTSSLHSGVPS 80
QY 42 RPSGSGSGTDFSTTSSLPQDFATYYC-----FGQGTGLEIK 79
DB 81 RPSGSGSGTDFSTTSSLPQDFATYYCQYRYLPWFPGGKLEIK 127

RESULT 14
Q8NEK1 PRELIMINARY; PRT; 234 AA.
AC Q8NEK1;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC030813; AAH30813.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_CI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;

Query Match 65.6%; Score 273; DB 4; Length 234;
Best Local Similarity 53.3%; Pred. No. 2e-24;
Matches 57; Conservative 12; Mismatches 10; Indels 28; Gaps 3;
QY 1 DIQMTQSPASISASVGDRTVITC-----WYLOKPQKSPQLIY-----GVPS 41
DB 21 EIVMTQSPATLSVSPGERATLSCRASQSVTSNLAWYQQTGQSPRLVITYGASSRSGVPA 80
QY 42 RPSGSGSGTDFSTTSSLPQDFATYYC-----FGQGTGLEIK 79
DB 81 RPSGSGSGTDFSTTSSLPQDFATYYCQYRYLPWFPGGKLEIK 127

RESULT 15
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8;
AC Q91WF8;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
```

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical 25.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AH15292.1; -.
DR InterPro; IPR03006; IG_MHC.
DR InterPro; IPR03596; IG_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E5EB7812D2 CRC64;

Query Match 64.7%; Score 269; DB 11; Length 234;
Best Local Similarity 56.1%; Pred. No. 6e-24;
Matches 60; Conservative 9; Mismatches 10; Indels 28; Gaps 4;

Qy 1 DIQWTQSPASLSASVGRVTITC-----WYLOKP-GKSPOLIY-----GVPS 41
Db 21 DIQWTQTSLSASLSGRVTISCRASODISNYLNWYQQKPDGTVKLLIYTSRLYLGVPS 80

Qy 42 RFGSGSGTDPSFTISSLPEDFATYYC-----FGQGTKLEIK 79
Db 81 RFGSGSGTDYSLTISNLEQEDLATYFCQQQNTPTPTFGSGTKLEVK 127

Search completed: January 13, 2004, 12:43:05
Job time : 17.1441 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 18.4218 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-79

Perfect score: 416

Sequence: 1 DIQMTSPASLSASVGRVT.....QPEDPATYTCFGQGTLEIK 79

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	376.5	90.5	80	ABG74720	Murine humanised M
2	337.5	81.1	19	AAW76130	Human ICR-1.1 V-K
3	337.5	81.1	110	AAW71260	Humanised murine a
4	337.5	81.1	110	AAW00786	Antibody against I
5	337.5	81.1	110	AAW81434	Humanised antibody
6	337.5	81.1	110	AAW13050	Humanised ICR-1.1
7	337.5	81.1	110	AAW32449	Humanised ICR-1.1
8	337.5	81.1	110	AAW50757	Humanised murine a
9	337.5	81.1	110	AAW70942	Humanised monoclon

10	335.5	80.6	126	21	AAW77599	Anti-human VEGF re
11	335.5	80.6	126	22	AAW78868	Anti-human FLT-1 a
12	335	80.5	110	13	AAW30147	431/26 VK hum. Sy
13	335	80.5	111	15	AAW47935	Humanised light ch
14	335	80.5	111	20	AAW89351	Humanised 23F2G 11
15	335	80.5	213	17	AAW04301	Antibody fusion pr
16	335	80.5	909	15	AAW50092	Humanised anti-CEA
17	334.5	80.4	107	15	AAW47222	Antibody light cha
18	334.5	80.4	107	18	AAW41397	Anti-CEA antibody
19	334.5	80.4	107	18	AAW41390	Anti-CEA antibody
20	334.5	80.4	107	24	ABP96012	HSA antibody relat
21	334.5	80.4	108	22	AAE12062	Human anti-tissue
22	334.5	80.4	125	16	AAW67656	Anti-human IL-6 ch
23	334.5	80.4	126	16	AAW89479	Anti-human IL-4 hu
24	334.5	80.4	128	21	AAW77597	Anti-human VEGF re
25	334.5	80.4	128	21	AAW78866	Anti-human FLT-1 a
26	334.5	80.4	212	23	AAU72815	DNA encoding TPA-8
27	334.5	80.4	232	16	AAW80616	Anti-human IL-4 hu
28	334.5	80.4	235	18	AAW41398	Humanised antibody
29	334.5	80.4	235	18	AAW41411	Humanised light ch
30	334.5	80.4	241	20	AAW21882	Amino acid sequenc
31	334	80.3	107	12	AAW11987	Human anti-placent
32	334	80.3	107	15	AAW55125	Mouse-human chimera
33	334	80.3	107	15	AAW60304	Chimeric anti HIV
34	334	80.3	107	19	AAW86804	Variable Light dom
35	334	80.3	107	19	AAW70623	Humanised murine a
36	334	80.3	107	20	AAW87455	Humanised anti-alp
37	334	80.3	107	22	AAW62085	Humanised Fab vers
38	334	80.3	107	22	AAW62087	Human V1 consensus
39	334	80.3	107	22	AAW60398	Humanised anti-Erb
40	334	80.3	107	22	AAW60400	Consensus human l1
41	334	80.3	107	22	AAW61583	Humanised Fab vers
42	334	80.3	107	22	AAW61585	Human variable lig
43	334	80.3	107	23	ABP61192	Humanised anti-VEG
44	334	80.3	107	24	ABW18721	Antibody library x
45	334	80.3	108	13	AAW70618	Anti-VEGF humanise

ALIGNMENTS

RESULT 1
ABG74720
ID ABG74720 standard; Protein; 80 AA.
XX
XX ABG74720;
XX
XX
DT 10-MAY-2003 (first entry)
DE Murine humanised Mu007-associated protein L1.

XX Murine; light chain; variable region; antibody; Crohn's disease;
XX human interleukin (IL)-1beta; antirheumatic; antiarthritic; humanised;
XX antinflammatory; osteopathic; antiallergic; cerebroprotective;
XX antiaschmatic; immunosuppressive; antibacterial; vaccine; Mu007;
XX rheumatoid arthritis; osteoarthritis; cartilage destruction;
XX allergy; septic shock; endotoxic shock; septicemia; stroke; asthma;
XX graft versus host disease; inflammatory bowel disease; LI.

XX Unidentified.
XX WO2003010282-A2.
XX
XX 06-FEB-2003.
XX

XX 18-JUL-2002; 2002WO-US21281.
XX
XX 26-JUL-2001; 2001US-307973P.
XX 14-AUG-2001; 2001US-312278P.
XX (ELIL) LILLY & CO ELI.
XX Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Teurushita N;
XX

PI Vasquez MJ;
 DR WPI; 2003-248068/24.
 XX
 XX New IL-beta antibodies, useful for treating allergy, septic or
 PT endotoxic shock, septicemia, stroke, asthma, graft versus host disease,
 PT Crohn's disease, or inflammatory bowel disease -
 XX
 PS Disclosure; Fig 1; 98pp; English.
 XX
 XX This invention describes a novel antibody that specifically binds mature
 CC human interleukin (IL)-beta, and binds the same epitope on mature human
 CC IL-beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
 CC The antibody of the invention have antirheumatic, antiarthritic,
 CC antiinflammatory, osteopathic, antiallergic, cerebroprotective,
 CC antitubercular, immunosuppressive and antibacterial activity and can be
 CC used in a vaccine. The antibody is useful for manufacturing a medicament
 CC for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
 CC cartilage destruction in a subject. The antibody is also useful for
 CC treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,
 CC graft versus host disease, Crohn's disease, or inflammatory bowel
 CC disease. This sequence represents a protein associated with the
 CC humanised murine Mu007 antibody described in the disclosure of the
 CC invention.
 XX
 SQ Sequence 80 AA;
 Query Match 90.5%; Score 376.5; DB 24; Length 80;
 Best Local Similarity 90.0%; Pred. No. 6.8e-27;
 Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 1 DIQMTQSPASLSASVGDRTVITTCWYLQKPKSPQ-LIYGVPRPSGSGGTDFTSSSL 59
 DB 1 DIQMTQSPASLSASVGDRTVITTCWYQKPKAPKSLIYGVPRPSGSGGTDFTLITSSL 60
 QY 60 QPEDFATYYCFGGQTKLEIK 79
 DB 61 QPEDFATYYCFGGQTKLEIK 80
 RESULT 2
 AAW76130
 ID AAW76130 standard; Protein; 110 AA.
 AC AAW76130;
 DT 20-NOV-1998 (first entry)
 XX Human ICR-1.1 V-K region PCR product protein.
 XX
 XX Interleukin adhesion molecule; human; ICAM-R; modulator; 14.3.3 family;
 KW HSI-beta; tubulin; inhibitor; stimulator; effector; immune response;
 KW inflammation; disorder; T cell activation; macrophage; Crohn's disease;
 KW adult respiratory distress syndrome; stroke; multiple sclerosis; asthma;
 KW rheumatoid arthritis; tumour growth; human immune deficiency virus;
 KW infection; diabetes; graft vs. host disease; passive immunisation.
 XX
 OS Homo sapiens.
 XX
 XX US5773218-A.
 XX
 XX 30-JUN-1998.
 XX
 XX 07-JUN-1995; 95US-0482882.
 XX
 XX 05-AUG-1994; 94US-0286754.
 XX
 XX 27-JAN-1992; 92US-0827689.
 XX
 XX 26-MAY-1992; 92US-0889724.
 XX
 XX 05-JUN-1992; 92US-0894061.
 XX
 XX 22-JAN-1993; 93US-0009266.
 XX
 XX 26-JAN-1993; 93WO-US000787.
 XX
 XX 05-AUG-1993; 93US-0102852.
 XX
 XX 07-JUN-1995; 95US-0482882.

XX
 PA (ICOS-) ICOS CORP.
 XX Gallatin WM, Vazeux R;
 PI
 XX WPI; 1998-386989/33.
 DR N-PSDB; AAV56428.
 DR
 XX Identifying compounds that modulate interaction of intercellular
 PT adhesion molecule R - with ligands HSI-beta and tubulin using
 PT two-hybrid assay, useful for treating inflammation, T cell
 PT activation etc.
 XX
 PS Example 13; Column 135-136; 108pp; English.
 XX
 XX This sequence represents a human ICR-1.1 V-K region amplified PCR
 CC product. This sequence is used in the isolation of a novel human
 CC intercellular adhesion molecule, ICAM-R. This sequence is used in a
 CC method which investigates modulators of the interaction between ICAM-R
 CC and the 14.3.3 family member HSI-beta and tubulin. An anti-ICAM-R
 CC antibody optionally coupled to toxin or radionuclide, or an ICAM-R
 CC peptide, can block, inhibit or stimulate ligand/receptor interactions
 CC involving ICAM-R, particularly its effector functions involved in
 CC (non)specific immune responses. ICAM-R related agents may be used to
 CC treat or monitor inflammation, disorders involving T cell activation or
 CC macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth,
 CC human immune deficiency virus infection, diabetes, graft vs. host disease
 CC and many others. Antibodies may also be used for passive immunisation,
 CC for purifying, detecting or quantifying ICAM-R and for identifying
 CC ICAM-R expressing cells.
 XX
 SQ Sequence 110 AA;
 Query Match 81.1%; Score 337.5; DB 19; Length 110;
 Best Local Similarity 88.9%; Pred. No. 3e-23;
 Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;
 QY 1 DIQMTQSPASLSASVGDRTVITTC-----WYLQKPKSPQ-LIY-----GVPSR 42
 DB 5 DIQMTQSPSSLSASVGDRTVITTCSSSVSYIYVQKPKAPKLLIYLTSLNLSGVPSR 64
 QY 43 FSGSGSGTDFPSITSLQPEDFATYYC-----FGGQTKLEIK 79
 DB 65 FSGSGSGTDFLTITSLQPEDFATYYCQOWKSIPLTFGGQTKLEIK 110
 RESULT 3
 AAW71260
 ID AAW71260 standard; Protein; 110 AA.
 XX
 XX AAW71260;
 AC
 XX 25-MAR-2003 (updated)
 DT 18-NOV-1998 (first entry)
 XX
 XX Humanised murine antibody ICR-1.1 light chain amino acid sequence.
 XX
 XX Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
 KW inflammatory condition; asthma; tumour growth; metastasis;
 KW viral infection; antibody ICR-1.1.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 XX US5811517-A.
 XX
 XX 22-SEP-1998.
 XX
 XX 07-JUN-1995; 95US-0483389.
 XX
 XX 05-AUG-1994; 94US-0286754.
 XX

PR 26-JAN-1993; 93WO-US00787.
 PR 27-JAN-1992; 92US-0827689.
 PR 28-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 05-AUG-1993; 93US-0102852.
 XX XX (ICOS-) ICOS CORP.
 XX PA
 XX Gallatin WM, Vazeux R;
 XX PI
 XX WPI; 1998-530940/45.
 DR N-PSDE; AAV54866.
 DR XX

XX DNA encoding mutant ICAM-R polypeptide(s) - useful for diagnosis
 PT and treatment of cell adhesion based disease conditions e.g.
 PT inflammation or asthma
 PT XX

XX Example 13; Columns 135-136; 111pp; English.
 XX PS

XX The present sequence represents the humanised light chain of murine
 CC antibody ICR-1.1. This antibody is specific for ICAM-R (intercellular
 CC adhesion molecule-R). ICAMs are polypeptides that are expressed on blood
 CC vessel endothelial cell surfaces and are involved in the adhesion events
 CC in various conditions. ICAM-R variants (see AAW71264-69) can be used to
 CC treat or monitor inflammatory conditions involving specific or
 CC nonspecific immune responses, asthma, tumour growth and/or metastasis
 CC and viral infections. The ICAM variants are produced recombinantly, from
 CC expression libraries of mutated sequences, and the ones that are
 CC claimed are the ones that have been found to be especially involved in
 CC adhesion events. They can also be used to raise antibodies, also for
 CC use as therapeutic or diagnostic agents.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC XX

XX Sequence 110 AA;
 XX SQ

Query Match 81.1%; Score 337.5; DB 19; Length 110;
 Best Local Similarity 68.9%; Pred. No. 3e-23; Indels 27; Gaps 4;
 Matches 73; Conservative 4; Mismatches 2

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42
 DB 5 DIQMTQSPSSLSASVGDRTVITCSASSSVSYIYWKQKPGKAPKLLIYLTSLASGVPSR 64
 QY 43 FSGSGSGTDFSTTSSLOPEDFATYYC-----FCQGTKLEIK 79
 DB 65 FSGSGSGTDFLTITSSLOPEDFATYYCQWKSIPLTFQGTKLEIK 110

RESULT 4
 AAY00786

ID AAY00786 standard; Protein; 110 AA.
 XX AC
 XX AAY00786;
 XX DT 14-MAY-1999 (first entry)
 XX DE Antibody against ICAM-R.

XX ICAM; immunoglobulin-like loop; intercellular adhesion molecule receptor;
 KW alpha d/CD18; antibody; immunisation; inflammatory response; asthma;
 KW tumour growth; viral infection; therapy.
 XX OS Mus sp.
 XX US5880268-A.
 XX PD 09-MAR-1999.
 XX PF 07-JUN-1995; 95US-0483932.
 XX PR 05-AUG-1994; 94US-0286754.
 PR 27-JAN-1992; 92US-0827689.

PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-US00787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1995; 95US-0483932.
 XX XX (ICOS-) ICOS CORP.
 XX PA
 XX Gallatin WM, Vazeux R;
 XX PI
 XX WPI; 1999-204041/17.
 DR N-PSDB; AAX21883.
 DR XX

XX New intercellular adhesion molecule receptor (ICAM-R) specific
 PT antibodies - useful for modulating ligand/receptor binding and
 PT biological activities involving ICAM-R, especially those of the
 PT specific and non-specific immune systems
 PT XX

XX Example 13; Column 135-136; 108pp; English.
 XX PS

XX This sequence represents an antibody specific for ICAM-R.
 CC The invention relates to antibodies (Ab) which bind specifically
 CC to the intercellular adhesion molecule receptor (ICAM-R), inhibiting the
 CC interaction between ICAM-R and alpha d/CD18. Abs with specific ICAM-R
 CC binding are useful in compositions for immunisation, and for purifying
 CC ICAM-R polypeptides and identifying cells expressing ICAM-R on their cell
 CC surface, modulating ligand/receptor binding and biological activities
 CC involving ICAM-R, especially inflammatory responses of the specific
 CC immune system, the non-specific immune system, monitoring and treating
 CC asthma, tumour growth, and/or metastasis, and viral infection (e.g. HIV
 CC infection). In particular diseases involving an essential T cell
 CC activation (e.g. asthma, psoriasis, diabetes, graft vs. host disease,
 CC tissue transplant rejection, and multiple sclerosis) may be treated with
 CC anti-ICAM-R antibodies. The Abs specifically bind to and identify ICAM-R
 CC and disrupt ICAM-R to cell adhesion molecule, especially alpha d/CD18
 CC binding.
 CC XX

XX Sequence 110 AA;
 XX SQ

Query Match 81.1%; Score 337.5; DB 20; Length 110;
 Best Local Similarity 68.9%; Pred. No. 3e-23; Indels 27; Gaps 4;
 Matches 73; Conservative 4; Mismatches 2

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42
 DB 5 DIQMTQSPSSLSASVGDRTVITCSASSSVSYIYWKQKPGKAPKLLIYLTSLASGVPSR 64
 QY 43 FSGSGSGTDFSTTSSLOPEDFATYYC-----FCQGTKLEIK 79
 DB 65 FSGSGSGTDFLTITSSLOPEDFATYYCQWKSIPLTFQGTKLEIK 110

RESULT 5
 AAW81454

ID AAW81454 standard; Protein; 110 AA.
 XX AC
 XX AAW81454;
 XX DT 17-FEB-1999 (first entry)
 XX DE Humanised antibody ICR-1.1 V κ region (HuVK).
 XX KW Inter-cellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;
 KW ICR-8.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour;
 KW graft-versus-host disease; viral infection; toxin; radionuclide;
 KW neovascularisation site.
 XX OS Mus sp.
 XX US5837822-A.
 XX PN
 XX XX

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PD 17-NOV-1998.
XX
XX 07-JUN-1995; 95US-0487113.
XX
XX 07-JUN-1995; 95US-0487113.
XX
XX 27-JAN-1992; 92US-0827689.
XX
XX 26-MAY-1992; 92US-0889724.
XX
XX 05-JUN-1992; 92US-0894061.
XX
XX 22-JAN-1993; 93US-0009266.
XX
XX 26-JAN-1993; 93WO-US00787.
XX
XX 03-AUG-1993; 93US-0102852.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX WPI; 1999-023535/02.
XX
XX N-PSDB; AAV69196.
XX
XX Humanised antibodies specific for intercellular adhesion molecule
XX polypeptide - useful for therapeutic or diagnostic purposes
XX
XX Example 13; Columns 145-148; 116pp; English.
XX
XX The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies
XX targeted to the human intercellular adhesion molecule polypeptide
XX (ICAM-R) polypeptide. Antibodies specific for ICAM-R's are potentially
XX useful as therapeutic compounds, for treating e.g. immune-mediated
XX inflammatory conditions (e.g. graft-versus-host disease), asthma,
XX tumours or viral infections. Monoclonal antibodies specific for ICAM-R,
XX or their conjugates formed with e.g. toxins or radionuclides are useful
XX for therapeutically targeting or detecting neovascularisation sites.
XX The present sequence represents the amino acid sequence of the V $\kappa$  region
XX of the humanised antibody ICR-1.1.
XX
XX Sequence 110 AA;
XX
XX Query Match 81.1%; Score 337.5; DB 20; Length 110;
XX Best Local Similarity 68.9%; Pred. No. 3e-23;
XX Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;
XX
XX 1 DIQMTQSPASLSASVGRVITTC-----WYLQKPGKSPQ-LIY-----GVPSR 42
XX 5 DIQMTQSPSSLSASVGRVITCSASSSVSYIYQKPKGPKLLIYLTSLNLSGVPSR 64
XX
XX 43 FSGSGSGTDFSTISSLPQDFATYYC-----FGQGTKLEIK 79
XX 65 FSGSGSGTDFTLTISLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
XX
XX RESULT 6
XX AAB13050
XX ID AAB13050 standard; Protein; 110 AA.
XX
XX AC AAB13050;
XX
XX 19-DEC-2000 (first entry)
XX
XX DE Humanised ICR-1.1 V $\kappa$  protein sequence.
XX
XX Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke;
XX intercellular adhesion molecule; immunoglobulin heavy chain; septicemia;
XX inflammatory conditions; glomerulonephritis; arthritis; dermatosis;
XX haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease;
XX necrotising enterocolitis; atherosclerosis; psoriasis; asthma;
XX transplant rejection; diabetes; tumour.
XX
XX Synthetic.
XX
XX OS US6100383-A.
XX
XX FN 08-AUG-2000.
XX
XX PD
XX

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PF 07-JUN-1995; 95US-0475680.
XX
XX 05-AUG-1994; 94US-0286754.
XX
XX 26-JAN-1993; 93WO-US00787.
XX
XX 27-JAN-1992; 92US-0827689.
XX
XX 26-MAY-1992; 92US-0889724.
XX
XX 05-JUN-1992; 92US-0894061.
XX
XX 22-JAN-1993; 93US-0009266.
XX
XX 05-AUG-1993; 93US-0102852.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gallatin WM, Vazeux R;
XX
XX WPI; 2000-542449/49.
XX
XX N-PSDB; AAA97170.
XX
XX Hybrid fusion proteins comprising intercellular adhesion molecule or
XX its variants useful, for treating inflammatory conditions, Crohn's
XX disease, atherosclerosis and diabetes
XX
XX Example 13; Column 135-138; 109pp; English.
XX
XX This invention relates to a hybrid fusion protein comprising an
XX intercellular adhesion molecule (ICAM-R) amino acid fragment at its
XX amino terminus and a constant domain of an immunoglobulin heavy chain at
XX its carboxy terminus. ICAM-R polypeptides are useful for treating and
XX monitoring inflammatory conditions such as adult respiratory distress
XX syndrome, multiple organ injury syndrome secondary to septicemia or
XX trauma, reperfusion injury of tissue, acute glomerulonephritis, reactive
XX arthritis, dermatosis, stroke, thermal injury, haemodialysis,
XX leukapheresis, ulcerative colitis, Crohn's disease, necrotising
XX enterocolitis, granulocyte transfusion associated syndrome,
XX atherosclerosis and cytokine induced toxicity. ICAM-R polypeptides are
XX also useful for treating conditions resulting from a response of the
XX specific immune system in a mammal e.g. psoriasis, organ/tissue
XX transplant rejection and autoimmune diseases including Raynaud's
XX syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid
XX arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R
XX related products are also useful in monitoring and treating asthma,
XX tumour growth and/or metastasis, and viral infection (e.g. HIV
XX infection). Sequences AAA97090 and AAB13036 represent the human ICAM-R
XX DNA and protein sequences. Sequences AAA97091-A97112 represent ICAM-R
XX DNA fragments, PCR primers and probes, all used in the identification of
XX the ICAM-R DNA sequence. AAA97113-A97123 and AAA97129-A97152 represent
XX primers used in the production of humanised anti-ICAM-R antibody ICR-8.1,
XX and fragments of the humanised antibody. Sequences AAA97124-A97128,
XX AAA97132, AAA97144 represent ICR-8.1 sequences. Sequences AAA97153-A97176
XX excluding AAA97155-A97156 represent primers used in the production of
XX humanised anti-ICAM-R antibody ICR-1.1, and fragments of the humanised
XX antibody. Sequences AAA97155-A97156 and AAB13047-B13048 represent murine
XX ICR-1.1 sequences. DNA and peptide sequences used in the production of
XX the chimeric protein of the invention include AAA97177-A97188 and
XX AAB13050-B13051.
XX
XX Sequence 110 AA;
XX
XX Query Match 81.1%; Score 337.5; DB 21; Length 110;
XX Best Local Similarity 68.9%; Pred. No. 3e-23;
XX Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;
XX
XX 1 DIQMTQSPASLSASVGRVITTC-----WYLQKPGKSPQ-LIY-----GVPSR 42
XX 5 DIQMTQSPSSLSASVGRVITCSASSSVSYIYQKPKGPKLLIYLTSLNLSGVPSR 64
XX
XX 43 FSGSGSGTDFSTISSLPQDFATYYC-----FGQGTKLEIK 79
XX 65 FSGSGSGTDFTLTISLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
XX
XX RESULT 7
XX AAY82449
XX ID AAY82449 standard; Protein; 110 AA.
XX

```


XX AC AAY82449;
 XX DT 28-JUN-2000 (first entry)
 XX DE Humanised ICR-1.1 antibody HuVK protein sequence SEQ ID NO:96.
 XX DE Human; ICAM-R; chromosome 19; intracellular adhesion molecule receptor;
 XX KW CAM; ICAM-1; ICAM-2; humanised; antibody; mutagenic; chimeric; vulnarary;
 XX KW nephropathic; antiarthritis; cerebroprotective; antitumor; cytosaric;
 XX KW antiarteriosclerotic; immunosuppressive; antidiabetic; neuroprotective;
 XX KW antihiv; dermatological; antiasthmatic; antiviral; antiinflammatory;
 XX KW anti-HIV; vasotropic; antipsoriatic; immunomodulator; antirheumatic;
 XX KW cell adhesion mediator; inflammatory condition; immunisation;
 XX KW immune response.
 XX OS Mus sp.
 XX OS Homo sapiens.
 XX PN US6040176-A.
 XX PD 21-MAR-2000.
 XX XX 12-SEP-1996; 96US-0714017.
 XX PR 05-AUG-1994; 94US-0286754.
 XX PR 27-JAN-1992; 92US-0827689.
 XX PR 26-MAY-1992; 92US-0889724.
 XX PR 05-JUN-1992; 92US-0894061.
 XX PR 22-JAN-1993; 93US-0009266.
 XX PR 26-JAN-1993; 93WO-US00787.
 XX PR 05-AUG-1993; 93US-0102852.
 XX XX (ICOS-) ICOS CORP.
 XX PI Gallatin WM, Vazeux R;
 XX DR WPI; 2000-270138/23.
 XX PT Novel monoclonal antibody directed against ICAM-R proteins useful for
 XX PT treating acute glomerulonephritis, ulcerative colitis, psoriasis,
 XX PT rheumatoid arthritis, diabetes, multiple sclerosis, asthma and viral
 XX PT infection -
 XX PS Example 13; Column 151-153; 117pp; English.
 XX CC The present invention describes a monoclonal antibody (MAB) (I),
 XX CC produced by the hybridoma cell line 81K2F (ATCC HB 11692). Also described
 XX CC are: (1) a hybridoma cell line 81K2F; and (2) a MAB (III), that competes
 XX CC with (1) for binding to ICAM-R (intracellular adhesion molecule
 XX CC receptor) (III). (II) mimics the activity of natural binding proteins
 XX CC through which intercellular and intracellular activities of (III) are
 XX CC modulated. (II) is also used for modulating the immune responses. (I) is
 XX CC used for immunisation as well as for purifying (III). They are also
 XX CC useful in modulating the ligand/receptor binding biological activity
 XX CC involving (III) especially those effector functions of (III) involved in
 XX CC specific and non-specific immune system responses. Inflammatory
 XX CC conditions which may be treated or monitored with related products of
 XX CC (III) include conditions resulting from a response of the non-specific
 XX CC immune system in a mammal e.g. adult respiratory distress syndrome,
 XX CC multiple organ injury syndrome secondary to septicemia or trauma,
 XX CC reperfusion injury of tissue, acute glomerulonephritis, reactive
 XX CC arthritis, stroke, ulcerative colitis and atherosclerosis, and conditions
 XX CC resulting from a response of the specific immune system in a mammal, e.g.
 XX CC psoriasis, organ/tissue transplantation rejection, autoimmune diseases
 XX CC such as autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,
 XX CC diabetes and lupus erythematosus. AAA08236 to AAA08334, and AAY82435 to
 XX CC AAY82451 represent sequences used in the exemplification of the present
 XX CC invention.
 XX XX Sequence 110 AA;
 XX SQ Query Match 81.1%; Score 337.5; DB 21; Length 110;

Best Local Similarity 68.9%; Pred. No. 3e-23;
 Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;
 QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPGKSPQ-LIY-----GVPSR 42
 DB 5 DIQMTQSPSSLSASVGDRTVITCASSSVSVIYVYQKPGKAPKLLIYLTNLSAGVPSR 64
 QY 43 FSGSGSGTDFPFTISSLPEDFATYYC-----FGQGTKLEIK 79
 DB 65 FSGSGSGTDFLTITISSLPEDFATYYCQWKSIPLTFGQGTKLEIK 110
 RESULT 8
 ID AAY50757 standard; Protein; 110 AA.
 XX AC AAY50757;
 XX DT 16-FEB-2000 (first entry)
 XX DE Humanised murine antibody ICR-1.1 VK protein.
 XX KW ICAM-R; murine; intercellular adhesion molecule; phosphorylation;
 XX KW protein kinase C; modulator; ICR-1.1; antibody.
 XX OS Synthetic.
 XX OS Mus sp.
 XX OS Homo sapiens.
 XX PN US5989843-A.
 XX PD 23-NOV-1999.
 XX XX 27-SEP-1996; 96US-0720420.
 XX PR 27-JAN-1992; 92US-0827689.
 XX PR 26-MAY-1992; 92US-0889724.
 XX PR 05-JUN-1992; 92US-0894061.
 XX PR 22-JAN-1993; 93US-0009266.
 XX PR 26-JAN-1993; 93WO-US00787.
 XX PR 05-AUG-1993; 93US-0102852.
 XX PR 07-JUN-1995; 95US-0487113.
 XX XX (ICOS-) ICOS CORP.
 XX PI Gallatin WM, Vazeux R;
 XX DR WPI; 2000-022778/02.
 XX DR N-PSDB; AA224342.
 XX PT Identifying modulators of protein kinase C phosphorylation of human
 XX PT intercellular adhesion molecule polypeptide -
 XX XX Example 14; Column 153-154; 122pp; English.
 XX CC This invention describes a novel method for identifying a compound that
 XX CC modulates phosphorylation of human intercellular adhesion molecule
 XX CC polypeptide (ICAM-R) by protein kinase C isoform. The method comprises:
 XX CC (a) exposing a purified peptide consisting of the cytoplasmic domain of
 XX CC ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in
 XX CC the presence and absence of a test compound; (b) measuring a labeled
 XX CC phosphate transferred to the peptide; and (c) identifying a test compound
 XX CC that affects transfer of the labeled phosphate as a modulator the
 XX CC The method is useful for identifying compounds that modulate the
 XX CC phosphorylation of human intercellular adhesion molecule polypeptide
 XX CC which might form the basis for the development of therapeutic and
 XX CC diagnostic agents. This sequence represents the humanised murine ICR-1.1
 XX CC antibody VK region which is used in the method of the invention.
 XX SQ Sequence 110 AA;
 XX Query Match 81.1%; Score 337.5; DB 21; Length 110;
 Best Local Similarity 68.9%; Pred. No. 3e-23;

Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY-----GVPSR 42
 Db 5 DIQMTQSPSLSASVGRVTITCSASSSVSYIYWQCKEKPAPKLLIYLTSLNLSGVPSR 64
 QY 43 FSGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
 Db 65 FSGSGSGTDFTLTISLQPEDFATYYCQWKSIPLTFGGQGTKLEIK 110

RESULT 9
 AAU70942
 ID AAU70942 standard; Protein; 110 AA.

XX
 AC AAU70942;
 XX
 DI 26-FEB-2002 (first entry)
 XX
 DE Humanised monoclonal antibody ICR-1.1 VK region.
 XX
 KW Human, intercellular adhesion molecule; ICAM; antiinflammatory; stroke;
 KW antibacterial; vulnery; vasotropic; nephrotropic; antiarthritic;
 KW cerebroprotective; dermatological; antiulcer; immunosuppressive; tumour;
 KW antipneumatic; antiarteriosclerotic; neuroprotective; antithyroid;
 KW virucide; antirheumatic; antidiabetic; antiaschmatic; cytostatic; asthma;
 KW hybridoma cell line; ATCC HB 12190; inflammation; septicaemia; trauma;
 KW adult respiratory distress syndrome; multiple organ injury syndrome;
 KW tissue reperfusion injury; acute glomerulonephritis; arthritis; vaccine;
 KW dermatosis; thermal injury; haemodialysis; leukopheresis; psoriasis;
 KW Crohn's disease; ulcerative colitis; multiple sclerosis; infection.
 XX
 OS Synthetic.
 XX
 PN US2001029293-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 03-JAN-2001; 2001US-0753436.
 XX
 PR 24-AUG-1999; 99US-0382289.
 PR 27-JAN-1992; 92US-0827689.
 PR 26-MAY-1992; 92US-0889724.
 PR 05-JUN-1992; 92US-0894061.
 PR 22-JAN-1993; 93US-0009266.
 PR 26-JAN-1993; 93WO-US00787.
 PR 05-AUG-1993; 93US-0102852.
 PR 07-JUN-1995; 95US-0487113.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gallatin WM, Vazeux R;
 XX
 DR WPI; 2002-009992/01.
 DR N-PSDB; ABK09359.
 XX
 PT Novel hybridoma cell line useful for producing monoclonal antibody for
 PT treating inflammatory conditions, immune system disorders and
 PT infectious diseases, is deposited under specified ATCC accession number
 PT -
 XX
 PS Page 83; Example 14; 126pp; English.
 XX
 CC The invention relates to a novel hybridoma cell line (I) ATCC HB 12190.
 CC (I) is useful for producing an intercellular adhesion molecule (ICAM)
 CC monoclonal antibody (II). (II) is useful for treating inflammatory
 CC conditions including adult respiratory distress syndrome, multiple organ
 CC injury syndrome secondary to septicemia or trauma, tissue reperfusion
 CC injury, acute glomerulonephritis, reactive arthritis, dermatosis with
 CC acute inflammatory components, stroke, thermal injury, haemodialysis,
 CC leukopheresis, ulcerative colitis, Crohn's disease, necrotising
 CC enterocolitis, granulocyte transfusion associated syndrome, diabetes,
 CC atherosclerosis, cytokine-induced toxicity, psoriasis, organ/tissue

CC transplant rejection, autoimmune diseases including Raynaud's syndrome,
 CC autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis,
 CC lupus erythematosus, asthma, tumour growth and/or metastasis, viral
 CC infection, tissue transplant rejection, graft versus host disease and
 CC multiple sclerosis. (II) is also useful for immunisation, for purifying
 CC ICAM-R polypeptides and for identifying cells that display the
 CC polypeptides on their surfaces. AAU70928-AAU70946 represent ICAM
 CC amino acid sequences of the invention.
 XX
 SQ Sequence 110 AA;

Query Match 81.1%; Score 337.5; DB 23; Length 110;
 Best Local Similarity 68.9%; Pred. No. 3e-23;
 Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY-----GVPSR 42
 Db 5 DIQMTQSPSLSASVGRVTITCSASSSVSYIYWQCKEKPAPKLLIYLTSLNLSGVPSR 64
 QY 43 FSGSGSGTDFSTTISLQPEDFATYYC-----FGQGTKLEIK 79
 Db 65 FSGSGSGTDFTLTISLQPEDFATYYCQWKSIPLTFGGQGTKLEIK 110

RESULT 10

AAU77599
 ID AAU77599 standard; peptide; 126 AA.

XX
 AC AAU77599;
 XX
 DT 08-MAY-2000 (first entry)
 XX
 DE Anti-human VEGF receptor Flt-1 antibody related peptide sequence #94.
 XX
 KW Antibody; human; vascular endothelial growth factor; VEGF receptor;
 KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
 KW rheumatoid arthritis; retinopathy; psoriasis.
 XX
 OS Mus musculus.
 XX
 PN WO9960025-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-JP02661.
 XX
 PR 20-MAY-1998; 98JP-0139000.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Shitara K, Ito M, Kawada Y, Nakamura K;
 XX
 DR WPI; 2000-072431/06.
 DR N-PSDB; AAZ87771.
 XX
 PT Gene recombinant antibodies, useful for diagnosis and as remedies for
 PT diseases due to abnormal neovascularization e.g. proliferation or
 PT metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
 PT and psoriasis -
 XX
 PS Claim 28; Page 202; 210pp; Japanese.
 XX
 CC The invention relates to a gene recombinant antibody that has specific
 CC reaction with human vascular endothelial growth factor (VEGF) receptor
 CC Flt-1. The antibodies are useful for diagnosis and as remedies for
 CC diseases due to abnormal neovascularisation such as proliferation or
 CC metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
 CC retinopathy, premature retinopathy and psoriasis.
 XX
 SQ Sequence 126 AA;

Query Match 80.6%; Score 335.5; DB 21; Length 126;
 Best Local Similarity 69.2%; Pred. No. 5.2e-23;

Matches 72; Conservative 5; Mismatches 2; Indels 25; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42
 Db 23 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 82
 QY 43 FSGSGGTDFTLTISLQPEDFATYYC-----FGQGTKLEIK 79
 Db 83 FSGSGGTDFTLTISLQPEDFATYYCHQWSMYTFGGTKVKEIK 126

RESULT 11
 AAB78868
 ID AAB78868 standard; Protein; 126 AA.
 XX
 AC AAB78868;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Anti-human Flt-1 antibody VL CDR protein sequence SEQ ID 90.
 XX
 KW Differentiation; monocyte; macrophage; haematopoietic stem cell; cancer;
 KW vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody;
 KW delayed hypersensitivity; malignant tumour; arteriosclerosis.
 XX
 OS Synthetic.
 XX
 FN WO200079275-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 16-JUN-2000; 2000WO-JP03957.
 XX
 PR 17-JUN-1999; 95JP-0171709.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 PI Shitara K, Shibuya M;
 XX
 XX WPI; 2001-080847/09.
 DR N-PSDB; AAF70244.
 XX

Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity -
 XX
 PS Example 3; Page 157; 164pp; Japanese.
 XX

This invention relates to a reagent for detecting differentiation of monocytes and macrophages from haematopoietic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEGF) receptor Flt-1. The invention also includes a method for diagnosing a disease in which the differentiation of monocytes and macrophages is implicated, using the reagent, and an agent for the treatment of diseases diagnosed using the method, containing a substance which binds to Flt-1 or a substance which inhibits the signal transduction of Flt-1. Diseases which may be diagnosed or treated include inflammation, delayed hypersensitivity, malignant tumours and arteriosclerosis.
 CC AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-human Flt-1 monoclonal antibody fragments, and
 CC oligonucleotides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AAF70245 - AAF78870 (excluding AAF70251) are used in the isolation of the antibody DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments of the anti-human Flt-1 antibody.
 CC
 XX Sequence 126 AA;
 SQ

Query Match 80.6%; Score 335.5; DB 22; Length 126;
 Best Local Similarity 69.2%; Pred. No. 5.2e-23;
 Matches 72; Conservative 5; Mismatches 2; Indels 25; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42

Db 23 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 82
 QY 43 FSGSGGTDFTLTISLQPEDFATYYC-----FGQGTKLEIK 79
 Db 83 FSGSGGTDFTLTISLQPEDFATYYCHQWSMYTFGGTKVKEIK 126

RESULT 12
 AAR30147
 ID AAR30147 standard; Protein; 110 AA.
 XX
 AC AAR30147;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-FEB-1993 (first entry)
 XX
 DE 431/26 VK hum.
 XX
 KW VH; VK; huTUMAK-L-beta-Gluc; monoclonal antibody; tumour; linker;
 KW beta-glucuronidase; hinge; prodrug.
 XX
 OS Synthetic.
 XX
 FN EP501215-A2.
 XX
 PD 02-SEP-1992.
 XX
 PF 10-FEB-1992; 92EP-0102197.
 XX
 PR 28-FEB-1991; 91DE-4106389.
 XX
 XX (BEHW) BEHRINGWERKE AG.
 PA (FARH) HOECHST AG.
 XX
 PI Bosslet K, Czech J, Hoffman D, Kolar C, Sedlacek H;
 PI Seemann G, Hoffmann D;
 XX
 DR WPI; 1992-293718/36.
 DR N-PSDB; AAQ26758.
 XX

Fusion protein for diagnosis and treatment - comprises humanised, tumour-specific monoclonal antibody (fragment), linker and beta-glucuronidase
 PT
 PT Disclosure; Page 19; 34pp; German.
 XX

The 431/26 VH and VK antibody fragments represented in AAQ26757-58 are pref. for the prodn. of the fusion proteins of formula huTUMAK-L-beta-Gluc (I) (huTUMAK= humanised, tumour-specific monoclonal antibody, or its tumour-binding fragments); L= linker; beta-gluc= human beta-glucuronidase). Betaglic Linker 1 and betaglic Linker 2 oligonucleotides are given in AAQ26759-60. Hinge 1 and hinge 2 oligonucleotides are given in AAQ26761-62.
 CC (I) are used to activate prodrugs. The antibody component provides for a specific targeting to tumours while the beta-gluc component activates a suitable prodrug by cleavage of glucuronic acid. The combination of the prodrug and (I) is useful in tumour treatment or diagnosis.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 110 AA;
 SQ

Query Match 80.5%; Score 335; DB 13; Length 110;
 Best Local Similarity 68.6%; Pred. No. 5.1e-23;
 Matches 72; Conservative 5; Mismatches 2; Indels 26; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLPKPKSPQ-LIY-----GVPSR 42
 Db 5 DIQMTQSPSSLSASVGDRTVITCSASSSVSYMHYQKPGKAPKLLIYRTSNLASGVPSR 64
 QY 43 FSGSGGTDFTLTISLQPEDFATYYC-----FGQGTKLEIK 79

Db 65 FGSFGSGTDTFTTISLQPEDATYYCHQWSSYPTFGQGTKEIK 109

RESULT 13
AAR47935
ID AAR47935 standard; Protein; 111 AA.

XX AAR47935;
AC
XX 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 24-JUL-1994 (first entry)
XX
XX Humanised light chain region of 23F2G.
XX Amplification; 23F2G; humanised antibody; heavy chain; light chain;
KW hybridoma; inflammation; CD18; human leukocyte integrins; mab 60.3;
KW monoclonal antibody; LFA-1; adhesion; migration; multiple
KW sclerosis; MS.

XX Mus sp.
OS Synthetic.

XX WO9402175-A1.

XX 03-FEB-1994.

XX 16-JUL-1993; 93WO-US06734.

XX 16-JUL-1992; 92US-0915068.

XX 10-MAY-1993; 93US-0060899.

XX (ICOS-) ICOS CORP.

XX (UNIW) UNIV WASHINGTON.

XX Rose LM;

XX WPI; 1994-048551/06.

XX N-PSDB; AAQ55917.

XX Antibodies immunologically reactive with the CD18 of human
PT leukocyte integrins and/or competing with mab 60.3 for binding to
PT human LFA-1 - for alleviating symptoms associated with
PT inflammatory disease states

XX Example 6; Page 45; 58pp; English.

XX Total RNA was isolated from the hybridoma cell line 23F2G and first
CC strand cDNA was synthesised using the total RNA as a template. The
CC first strand cDNA was used as a template for PCR to obtain double
CC stranded DNA fragments encoding the variable regions of both the
CC heavy and light chains of monoclonal antibody 23F2G. The sequence
CC shown is a humanised form of the light chain variable region of MAb
CC 23F2G. The humanised form of MAb 23F2G may be administered to
CC alleviate symptoms associated with inflammatory disease states, esp.
CC for the inhibition of inflammatory processes associated with
CC multiple sclerosis. The MAb blocks leukocyte adhesion and
CC migration to inflammatory sites. The MAb is an anti-CD18 integrin
CC antibody which competes with MAb 60.3 for binding to LFA-1.
CC See also AAR47931-6.
CC (Updated on 10-MAR-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 111 AA;

Query Match 80.5%; Score 335; DB 15; Length 111;

Best Local Similarity 65.8%; Pred. No. 5.1e-23;

Matches 73; Conservative 4; Mismatches 2; Indels 32; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY----- 37

Db 1 DIQMTQSPSSLSASVGDRTVITCRASERVESYGNFMWYQKPKAPKLLIYPSNLQS 60

QY 38 GVPSPFSGSGGTDFSTFTTISLQPEDFATYYC-----FGQGTKEIK 79
Db 61 GVPSPFSGSGGTDFSTFTTISLQPEDFATYYCHQDNEPPTFGQGTKEIK 111

RESULT 14

AAW89351
ID AAW89351 standard; Protein; 111 AA.

XX AAW89351;

XX 02-MAR-1999 (first entry)

XX Humanised 23F2G light chain variable region.

XX Mouse; humanised; antibody; heavy chain variable region; light chain;
KW 23F2G; inflammatory disease; multiple sclerosis; common beta chain;
KW CD18; human leukocyte integrin.

XX Mus sp.

XX Homo sapiens.

XX Synthetic.

XX US5854070-A.

XX 29-DEC-1998.

XX 21-JAN-1997; 97US-0785571.

XX 16-JUL-1993; 93US-0094535.

XX 16-JUL-1992; 92US-0915068.

XX 10-MAY-1993; 93US-0060699.

XX 28-FEB-1995; 95US-0396089.

XX 21-JAN-1997; 97US-0785571.

XX (ICOS-) ICOS CORP.

XX (UNIW) UNIV WASHINGTON.

XX Rose LM;

XX WPI; 1999-094920/08.

XX N-PSDB; AAV81909.

XX Hybridomas that secrete anti-CD18 antibody - useful for treating
PT inflammation specifically multiple sclerosis

XX Example 6; Column 27-30; 24pp; English.

XX The present invention describes the hybridoma cell line 23F2G
CC (ATCC HB 11801) and the Chinese hamster ovary (CHO) cell lines 636
CC (ATCC CRL 11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (Mab)
CC 23F2G (and its humanised variants 6E6 and B13-24) is an anti-human CD18
CC antibody for the treatment of inflammation, specifically multiple
CC sclerosis. The present sequence represents humanised 23F2G light chain
CC variable region from the present invention.

XX Sequence 111 AA;

Query Match 80.5%; Score 335; DB 20; Length 111;

Best Local Similarity 65.8%; Pred. No. 5.1e-23;

Matches 73; Conservative 4; Mismatches 2; Indels 32; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY----- 37

Db 1 DIQMTQSPSSLSASVGDRTVITCRASERVESYGNFMWYQKPKAPKLLIYASNLQS 60

QY 38 GVPSPFSGSGGTDFSTFTTISLQPEDFATYYC-----FGQGTKEIK 79

Db 61 GVPSPFSGSGGTDFSTFTTISLQPEDFATYYCHQDNEPPTFGQGTKEIK 111

RESULT 15

```

AAW04301
ID AAW04301 standard; Protein; 213 AA.
XX
AC AAW04301;
XX
DT 25-MAR-2003 (updated)
DT 14-FEB-1997 (first entry)
XX
DE Antibody fusion protein..
XX
KW Antibody; fusion protein; recombinant antibody; tumour therapy;
KW prodrug.
XX
OS Synthetic.
XX
PN EP737747-A2.
XX
PD 16-OCT-1996.
XX
PF 13-MAR-1996; 96EP-0103913.
XX
PR 11-APR-1995; 95DE-1013676.
XX.
PA (BEHW ) BEHRINGWERKE AG.
XX
PI Bosslet K, Czech J, Oppen M;
XX
DR WPI; 1996-457328/46.
DR N-PSDB; AAT38397.
XX
PT Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion
PT protein - by cytoplasmic expression in thio:redoxin:reductase
PT deficient E. coli
XX
PS Example 1; Figure 5a; 12pp; German.
XX
CC production of recombinant antibodies (Ab), Ab fragments or Ab
CC fragment/enzyme fusion proteins can be used for tumour therapy,
CC especially when the fusion protein comprises a tumour-specific
CC Ab fragment and an enzyme capable of converting a non-toxic prodrug
CC to a toxic drug. The fusion proteins are constructed in expression
CC vectors and expressed in thio:redoxin:reductase deficient E.coli,
CC allowing expression products to be isolated in soluble functional
CC form without renaturation. The Ab fragment is an FAb fragment or an
CC antigen binding region. In the fusion protein, the Ab component is
CC humanised and the enzyme component is a human cytoplasmic enzyme.
CC This fusion protein comprises the antibody constant and variable
CC light chain regions.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 213 AA;

Query Match      80.5%; Score 335; DB 17; Length 213;
Best Local Similarity 68.6%; Pred.No.9.4e-23;
Matches 72; Conservative 5; Mismatches 2; Indels 26; Gaps 4;

QY 1 DIQMTQSPASISASVGDRTITC-----WYLPKPKSPQ-LIY-----GVPSR 42
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DIQMTQSPSSLSASVGDRAVITCTSSSVSYMHVYQKPKGKAPKLLIYSTNLSAGVPSR 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 43 FSGSGSGTDFTTISLSLOPEFATYYC-----FGQGTKLEIK 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 FSGSGSGTDFTTISLSLOPEDIATYYCHQWSSYPTFGQGTKVEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: January 13, 2004, 12:38:23
Job time : 19.4218 secs

```



```
Best Local Similarity 90.0%; Pred. No. 1.5e-29;
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGTDFSTFISL 59
Db 1 DIQMTQSPSLSASVGDRTVITCWYLOKPGKAPKLLIYGVPSRFSGSGTDFSTFISL 60
QY 60 QPEDFATYYCFGQGTKEIK 79
Db 61 QPEDATYYCFGQGTKEIK 80

RESULT 2
US-08-765-783A-104
; Sequence 104, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-104

Query Match 90.7%; Score 377.5; DB 2; Length 80;
Best Local Similarity 90.0%; Pred. No. 1.5e-29;
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGTDFSTFISL 59
Db 1 DIQMTQSPSLSASVGDRTVITCWYLOKPGKAPKLLIYGVPSRFSGSGTDFSTFISL 60
QY 60 QPEDFATYYCFGQGTKEIK 79
Db 61 QPEDATYYCFGQGTKEIK 80
```

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RESULT 3
US-09-205-231-85
; Sequence 85, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SAITO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-205-231-85

Query Match 90.7%; Score 377.5; DB 3; Length 80;
Best Local Similarity 90.0%; Pred. No. 1.5e-29;
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITCWYLOKPGKSPQ-LIYGVPSRFSGSGTDFSTFISL 59
Db 1 DIQMTQSPSLSASVGDRTVITCWYLOKPGKAPKLLIYGVPSRFSGSGTDFSTFISL 60
QY 60 QPEDFATYYCFGQGTKEIK 79
Db 61 QPEDATYYCFGQGTKEIK 80

RESULT 4
US-09-416-557-104
; Sequence 104, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiaki
```


APPLICANT: Sato, Koh
APPLICANT: Teuchiya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,557
FILING DATE: 12-October-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,783
FILING DATE: 7-March-1997
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-416-557-104

Query Match 90.7%; Score 377.5; DB 3; Length 80;
Best Local Similarity 90.0%; Pred. No. 1.5e-29;
Matches 72; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 DIQMTSPASLSASVGDRTVITTCWYQKPKSPQ-LIYGVPSRFGSGSGTDFSTISL 59
Db 1 DIQMTSPSLSASVGDRTVITTCWYQKPKAPKLLIYGVPSRFGSGSGTDFSTISL 60

QY 60 QPEDFATYYCFQGQTKLEIK 79
Db 61 QPEDATYYCFQGQTKVEIK 80

RESULT 5
US-08-646-265A-112
Sequence 112, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-112

Query Match 87.5%; Score 364; DB 3; Length 87;
Best Local Similarity 82.9%; Pred. No. 3.3e-28;
Matches 72; Conservative 5; Mismatches 2; Indels 8; Gaps 2;

QY 1 DIQMTSPASLSASVGDRTVITTCWYQKPKSPQ-LIY-----GVPSRFGSGSGTDF 52
Db 1 DIQMTSPSLSASVGDRTVITTCWYQKPKAPKLLIYASVPSRFGSGSGTDF 60

QY 53 SFTISSLQPEDFATYYCFQGQTKLEIK 79
Db 61 TFTISSLQPEDATYYCFQGQTKVEIK 87

RESULT 6
US-08-554-840-10
Sequence 10, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADIAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 3; Length 80;
Best Local Similarity 85.0%; Pred. No. 1e-27;
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79
DB 61 QSDDFATYYCFGQGTKEIK 80

US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 4; Length 80;
Best Local Similarity 85.0%; Pred. No. 1e-27;
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79
DB 61 QSDDFATYYCFGQGTKEIK 80

US-08-554-840-10

RESULT 8
US-09-332-595-10
Sequence 10, Application US/09332595
Patent No. 6506383
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,595
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-332-595-10

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 3; Length 80;
Best Local Similarity 85.0%; Pred. No. 1e-27;
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79
DB 61 QSDDFATYYCFGQGTKEIK 80

US-08-554-840-10

Query Match 86.2%; Score 358.5; DB 3; Length 80;
Best Local Similarity 85.0%; Pred. No. 1e-27;
Matches 68; Conservative 8; Mismatches 3; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGDRTVITTCWYQKPGKSPQ-LIYGVPFRFSGSGGTDFSTISL 59
DB 1 DIQMTQSPSTLSASVGDRTVITTCWYQKPGKAPKVLIIYGVPSRFGSGGTFTLTISL 60

QY 60 QPEDFATYYCFGQGTKEIK 79
DB 61 QSDDFATYYCFGQGTKEIK 80

US-08-554-840-10

RESULT 7
US-08-925-339-10
Sequence 10, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-925-339-10

```
RESULT 9
US-08-554-840-12
; Sequence 12, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-554-840-12

Query Match 84.0%; Score 349.5; DB 3; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGRVTITCWYLOKPGKSPQ-LIYGVPSPRSGSGGTDFSTISL 59
Db 1 DIVMTQSPFLSASVGRVTITCWYQKPGKPKLLIYGVPDRFSGSGGTDFLTISL 60

QY 60 QPEDFATYVCFGGGKLEIK 79
Db 61 QPEDFADYFCFGGKLEIK 80

RESULT 10
US-08-925-339-12
; Sequence 12, Application US/08925339
; Patent No. 6440418
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
```

```
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,339
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-925-339-12

Query Match 84.0%; Score 349.5; DB 4; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1 DIQMTQSPASLSASVGRVTITCWYLOKPGKSPQ-LIYGVPSPRSGSGGTDFSTISL 59
Db 1 DIVMTQSPFLSASVGRVTITCWYQKPGKPKLLIYGVPDRFSGSGGTDFLTISL 60

QY 60 QPEDFATYVCFGGGKLEIK 79
Db 61 QPEDFADYFCFGGKLEIK 80

RESULT 11
US-09-332-595-12
; Sequence 12, Application US/09332595
; Patent No. 6506383
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: HANNA, Nabil
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39.
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/332,595
; FILING DATE:
; CLASSIFICATION:
```

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/554,840
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-127
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 80 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-332-595-12

Query Match 84.0%; Score 349.5; DB 4; Length 80;
Best Local Similarity 85.0%; Pred. No. 7.3e-27;
Matches 68; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DIQWTQSPASLSASVGRVTITCWYLQKPKSPQ-LIYGVPSPFSGSGTDFPSFTISL 59
Db 1 DIVNTQSPFLSASVGRVTITCWYQKPKSPKLLIYGVPDRFSGSGTDFTLTISL 60

Qy 60 QPEDFATYFCGGGTGLEIK 79
Db 61 QPEDFADYFCGGGTGLEIK 80

RESULT 12
US-08-553-501A-87
; Sequence 87, Application US/08553501A
; Patent No. 5856135
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AOAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

;; INFORMATION FOR SEQ ID NO: 87:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-553-501A-87

Query Match 83.1%; Score 345.5; DB 2; Length 98;
Best Local Similarity 72.4%; Pred. No. 2.2e-26;
Matches 71; Conservative 6; Mismatches 2; Indels 19; Gaps 3;

Qy 1 DIQWTQSPASLSASVGRVTITC-----WYLOKPKSPQ-LIY-----GVPS 41
Db 1 DIQWTQSPFLSASVGRVTITCRASNIYSNLAWYQKPKAPKLLIYAATYVLADGVPS 60

Qy 42 RFGSGSGTDFPSFTISLQPEDFATYFCGGGTGLEIK 79
Db 61 RFGSGSGTDFPSFTISLQPEDFATYFCGGGTGLEIK 98

RESULT 13
US-09-205-231-87
; Sequence 87, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AOAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-205-231-87

Query Match 83.1%; Score 345.5; DB 3; Length 98;

Best Local Similarity 72.4%; Pred. No. 2.2e-26;
Matches 71; Conservative 6; Mismatches 2; Indels 19; Gaps 3;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 41

Db 1 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPS 60

QY 42 RFGSGSGTDFSTFISSLOPEDFATYYCFGGTKLEIK 79

Db 61 RFGSGSGTDFSTFISSLOPEDFATYYCFGGTKVEIK 98

RESULT 14

US-08-482-882-96

Sequence 96, Application US/08482882

Patent No. 5773218

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 116

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,882

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,754

FILING DATE:

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5773218and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 32178

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-482-882-96

Query Match 81.1%; Score 337.5; DB 1; Length 110;

Best Local Similarity 68.9%; Pred. No. 1.4e-25;

Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42

Db 5 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 64

QY 43 RFGSGSGTDFSTFISSLOPEDFATYYC-----FGGTKLEIK 79

Db 65 RFGSGSGTDFSTFISSLOPEDFATYYCQWKSIPLTFGGTKLEIK 110

RESULT 15

US-08-483-389-96

Sequence 96, Application US/08483389

Patent No. 5811517

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-RELATED PROTEIN

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive/6300 Sears Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,389

FILING DATE: 07-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Sub, Young J.

REGISTRATION NUMBER: P-41,337

REFERENCE/DOCKET NUMBER: 27866/32760

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: (312) 474-6600

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 110 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-483-389-96

Query Match 81.1%; Score 337.5; DB 2; Length 110;

Best Local Similarity 68.9%; Pred. No. 1.4e-25;

Matches 73; Conservative 4; Mismatches 2; Indels 27; Gaps 4;

QY 1 DIQMTQSPASLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 42

Db 5 DIQMTQSPSSLSASVGDRTVITC-----WYLOKPKSPQ-LIY-----GVPSR 64

Qy 43 FSGSGTDFSTISSLOPEDPATYIC-----FGGTKLEIK 79
Db 65 FSGSGTDFSTISSLOPEDPATYICQOWKSIPLTFFGGTKLEIK 110

Search completed: January 13, 2004, 12:46:32
Job time : 7.83057 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 6.30655 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASVRV.....DTAVFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345.5	77.1	119	2 A24672	Ig heavy chain pre
2	343.5	76.7	469	2 S37483	Ig gamma-2a chain
3	341	76.1	138	2 S21810	Ig heavy chain v r
4	340	75.9	246	2 S38950	Ig gamma chain m
5	340	75.9	446	2 S40295	Ig gamma-2a chain
6	339.5	75.8	137	2 H32513	Ig heavy chain pre
7	337.5	75.3	120	2 B22769	Ig heavy chain v r
8	337.5	75.3	141	2 J10076	Ig heavy chain pre
9	337	75.2	116	2 S55542	Ig heavy chain v r
10	337	75.2	119	2 PH0961	Ig heavy chain v r
11	336.5	75.1	120	2 S41394	Ig heavy chain v r
12	335.5	74.9	116	2 S33751	Ig heavy chain v r
13	335.5	74.9	122	2 PH0958	Ig heavy chain v r
14	335.5	74.9	139	1 MMS18	Ig heavy chain pre
15	335.5	74.9	287	4 PC4402	peB leader/Ig hea
16	334.5	74.7	118	2 S36265	Ig heavy chain v r
17	334.5	74.7	119	2 P30502	Ig heavy chain v r
18	333.5	74.4	118	2 C30560	Ig heavy chain v r
19	333	74.3	119	2 S20640	Ig heavy chain v r
20	332.5	74.2	115	2 A54378	Ig heavy chain v r
21	332.5	74.2	116	2 PH0959	Ig heavy chain v r
22	332.5	74.2	136	2 J10077	Ig heavy chain pre
23	332.5	74.2	136	2 PH0960	Ig heavy chain v r
24	332	74.1	121	2 H37266	Ig heavy chain v r
25	331.5	74.0	115	2 P30238	Ig heavy chain v r
26	331.5	74.0	118	2 S38717	Ig heavy chain v r
27	331.5	74.0	139	2 PS0024	Ig heavy chain pre
28	331	73.9	142	2 A32483	Ig heavy chain v r
29	330.5	73.8	120	2 G38195	Ig heavy chain v r

30	330.5	73.8	120	2 PH0962	Ig heavy chain v r
31	330.5	73.8	128	2 PH0952	Ig heavy chain v r
32	330.5	73.8	132	2 PH0954	Ig heavy chain v r
33	330	73.7	138	2 E32513	Ig heavy chain pre
34	329.5	73.5	137	1 G2MS43	Ig heavy chain pre
35	329.5	73.5	139	2 A27609	Ig heavy chain v r
36	329	73.4	117	1 MEMS4E	Ig heavy chain v r
37	329	73.4	117	1 MEMS35	Ig heavy chain v r
38	329	73.4	121	2 F37266	Ig heavy chain v r
39	329	73.4	127	2 PH0955	Ig heavy chain v r
40	329	73.4	140	2 T01407	Ig heavy chain (my
41	328	73.2	119	2 S03077	Ig heavy chain v r
42	328	73.2	120	2 S25175	Ig heavy chain v r
43	328	73.2	123	2 S20645	Ig heavy chain v r
44	328	73.2	136	2 P10208	Ig heavy chain pre
45	327.5	73.1	120	2 F28195	Ig heavy chain v r

ALIGNMENTS

RESULT 1

A24672 Ig heavy chain precursor V region (VNU-3.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C;Accession: A24672

R;Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A;Reference number: A91022; MUID:86055722; PMID:2998759

A;Accession: A24672

A;Molecule type: DNA

A;Residues: 1-119 <WIN>

A;Cross-references: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:G773578

A;Note: this sequence was determined from the germline gene

C;Superfamily: Immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;4-119/Product: Ig heavy chain V region VNU-3.2 #status predicted <MAT>

F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 345.5; DB 2; Length 119;

Best Local Similarity 62.1%; Pred. No. 5.4e-27;

Matches 72; Conservative 10; Mismatches 5; Indels 29; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSKASGYST-----WVRQSPGKGLW----- 43

Db 4 QYQLQSGFELVKPGASVKISCKASGYAFSSMMNWKQRPCKGLEWIGRIYPGDITNY 63

Qy 44 -----GKALTVDKSTSTAYMELSLRSEDITAYFCAR-----WGQTTTVSS 87

Db 64 NGKFKGKATLTADKSSSTAYMQLSLSLTSDSAVYFCARDYGYGSDYWGQTTTVSS 119

RESULT 2

S37483

Ig gamma-2a chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37483

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37483

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-469 <DUC>

A;Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PID:G406253

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 343.5; DB 2; Length 469;

Best Local Similarity 60.8%; Pred. No. 3.3e-26;

```
Matches 73; Conservative 9; Mismatches 5; Indels 33; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSQPGKGLWV----- 43
Db 20 QIQLQSQGPELVKPGASVRVSCASGYSTFYDYYIHWVKQPGGLEWIGWIYVPSGNTKY 79
Qy 44 -----GKATLTVDKSTSTAYMELSSLSRSEDYAVFCAR-----WGQGTITVTSS 87
Db 80 NENFKGKATLTVDTSSTAYMQLSSLTSEDYAVFCARANGATALLDYGQGTITVTSS 139

RESULT 3
S21810
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21810
R:Ostermeyer, M.; Brack, C.H.; Trauneker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain
A:Reference number: S21810
A:Accession: S21810
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:G54163; PIDN:CAA40257.1; PID:G54164
C:Genetics:
A:Introns: 15/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 341; DB 2; Length 138;
Best Local Similarity 60.5%; Pred. No. 1.7e-26;
Matches 72; Conservative 9; Mismatches 6; Indels 32; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSQPGKGLWV----- 43
Db 20 QVQLQSQGPELVKPGASVRVSCASGYSTFYDYYIHWVKQPGGLEWIGWIYVPSGNTKY 79
Qy 44 -----GKATLTVDKSTSTAYMELSSLSRSEDYAVFCAR-----WGQGTITVTSS 87
Db 80 NENFKGKATLTADKSSSTAYMQLSSLTSEDYAVFCARNGYSSYGLAYWGQGTITVTSS 138

RESULT 4
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A>Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 340; DB 2; Length 246;
Best Local Similarity 61.5%; Pred. No. 3.8e-26;
Matches 72; Conservative 10; Mismatches 5; Indels 30; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSQPGKGLWV----- 43
Db 1 QIQLQSQGPELVKPGASVRVSCASGYSTFYDYYIHWVKQPGGLEWIGWIYVPSGNTKY 60
Qy 44 -----GKATLTVDKSTSTAYMELSSLSRSEDYAVFCAR-----WGQGTITVTSS 87
Db 61 NENFKGKATLTVDTSSTAYMQLSSLTSEDYAVFCARGGKAFMDYWGQGTITVTSS 117

RESULT 5
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B. submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MA>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224, 227, 229/Disulfide bonds: interchain #status predicted
F:229/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 75.9%; Score 340; DB 2; Length 446;
Best Local Similarity 61.5%; Pred. No. 6.9e-26;
Matches 72; Conservative 10; Mismatches 5; Indels 30; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSQPGKGLWV----- 43
Db 1 QIQLQSQGPELVKPGASVRVSCASGYSTFYDYYIHWVKQPGGLEWIGWIYVPSGNTKY 60
Qy 44 -----GKATLTVDKSTSTAYMELSSLSRSEDYAVFCAR-----WGQGTITVTSS 87
Db 61 NENFKGKATLTVDTSSTAYMQLSSLTSEDYAVFCARGGKAFMDYWGQGTITVTSS 117

RESULT 6
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: H32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988
A>Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94689; MUID:88331394; PMID:3138286
A:Accession: H32513
A:Molecule type: DNA
A:Residues: 1-137 <KOF>
A:Cross-references: GB:M20831; NID:G196949; PIDN:AAA38848.1; PID:G196950
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:134-117/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 339.5; DB 2; Length 137;
Best Local Similarity 61.0%; Pred. No. 2.4e-26;
Matches 72; Conservative 10; Mismatches 5; Indels 31; Gaps 3;

Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVRSQPGKGLWV----- 43
Db 20 EIQLOQSGAELVKPGASVRVSCASGYSTFYDYYIHWVKQPGGLEWIGWIYVPSGNTKY 79
```



```
QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVTSS 87
Db 80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYVCARKNYGSSFDYWGQGTITVTSS 137

RESULT 7
B22769
IG heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Didrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: B22769
A:Molecule type: protein
A:Residues: 1-120 <DI>
A>Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 337.5; DB 2; Length 120;
Best Local Similarity 59.2%; Pred. No. 3.3e-26;
Matches 71; Conservative 10; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRSCKASGYST-----WVRSQPKGLEWIG----- 43
Db 1 QVQLQPGALVKPGASVKVKSCASGYSTFTSWMHVWVKQRPQGQLEWIGRIHPDSDTNY 60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVTSS 87
Db 61 NQKFKGKATLTVDKPSSTAYMQLNSLTSEDSAVYVCARYDYGSYFDYWGQGTITVTSS 120

RESULT 8
JL0076
IG heavy chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: JL0076
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-react
A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0076
A:Molecule type: mRNA
A:Residues: 1-141 <KAA>
A:Cross-references: GB:M27788; NID:g195851; PIDN:AAA38441.1; PID:g195852
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-141/Product: Ig heavy chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:50-54/Region: complementarity-determining 1
F:69-85/Region: complementarity-determining 2
F:123-135/Region: complementarity-determining 3
F:136-141/Region: C

Query Match 75.3%; Score 337.5; DB 2; Length 141;
Best Local Similarity 60.3%; Pred. No. 3.9e-26;
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRSCKASGYST-----WVRSQPKGLEWIG----- 44
Db 20 QVQLQPGALVKPGASVKLSCKASGYSTFTSWMHVWVKQRPQGQLEWIGRIDPNSGGTKY 79

QY 45 -----KATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVTSS 87
Db 80 NEKFKSKATLTVDKPSSTAYMQLNSLTSEDSAVYVCAREGPDYWGQGTITVTSS 135
```

```
RESULT 9
S55542
IG heavy chain V region pe2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55542
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55542
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOE>
A:Cross-references: EMBL:X82581; NID:g854302; PIDN:CAA57917.1; PID:g854303
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 337; DB 2; Length 116;
Best Local Similarity 60.3%; Pred. No. 3.6e-26;
Matches 70; Conservative 11; Mismatches 5; Indels 30; Gaps 3;

QY 2 IQLVSGGELVKPGASVRSCKASGYST-----WVRSQPKGLEWIG----- 44
Db 1 VQLQSGALVKPGASVKLSCKASGYSTFTRYVMVWVKQRPQGQLEWIGINPSNGGTNFN 60

QY 45 -----KATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVTSS 87
Db 61 EKFKSKATLTVDKSSSTAYMQLNSLTSEDSAVYVTRGVASMDYWGQGTITVTSS 116

RESULT 10
PH0961
IG heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffv, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 993-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0961
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <NAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-107/Region: complementarity-determining 3

Query Match 75.2%; Score 337; DB 2; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.7e-26;
Matches 69; Conservative 13; Mismatches 5; Indels 32; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRSCKASG-----YSFTVWRQSPKGLEWIG----- 43
Db 1 QVQLVSGAELVKPGSVSVKSCASGTTSSVAISHWVQRPQGQLEWIGGIPIFTANY 60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQGTITVTSS 87
Db 61 AQKFGKATLTVDKSTAYMELSLRSRSDTAVYVCARGVYVYGVMDVWGQGTITVTSS 119

RESULT 11
S41394
```

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S41394
R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN
A:Reference number: S41393
A:Accession: S41394
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MAR>
A:Cross-references: EMBL:Z29586; NID:G452354; PIDN:CAA82703.1; PID:G1334080
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMW>
Query Match 75.1%; Score 336.5; DB 2; Length 120;
Best Local Similarity 58.3%; Pred. No. 4.1e-26;
Matches 70; Conservative 12; Mismatches 5; Indels 33; Gaps 3;
Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVROSPGKGLWEI----- 43
Db 1 EVQLQSGGELVKPGASVKLSKASGYTFTSYMHVWVKRPGQGLEWIGEIDPSDSTYY 60
Qy 44 -----GKATLTVDKSTSTAYMESSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
Db 61 NQKFKGKATLTVDKSSSTAYMQSSLTSDSAVYCARRYGSRVSMYWGQGTITVTVSS 120
RESULT 12
S53751
antibody Fab Jcl 103 heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
C:Accession: S53751
R:Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A:Title: Preparation, characterization and crystallization of an antibody Fab fragment
A:Reference number: S53750; MUID:95018269; PMID:7523684
A:Accession: S53751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <POK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMW>
Query Match 74.9%; Score 335.5; DB 2; Length 116;
Best Local Similarity 60.3%; Pred. No. 5e-26;
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;
Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVROSPGKGLWEI----- 43
Db 1 QVQLQSGGELVKPGASVKLSKASGYTFTSYMQWVKRPGQGLEWIGEIDPSDSTYY 60
Qy 44 -----GKATLTVDKSTSTAYMESSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
Db 61 NQKFKGKATLTVDSSSTAYMQSSLTSDSAVYCANLRGYDYGQGTITVTVSS 116
RESULT 13
PH0958
Ig heavy chain V region (G6+ CUL-HUR) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0958
R:Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0958
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA

A:Residues: 1-122 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMW>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-110/Region: complementarity-determining 3
Query Match 74.9%; Score 335.5; DB 2; Length 122;
Best Local Similarity 56.6%; Pred. No. 5.3e-26;
Matches 69; Conservative 13; Mismatches 5; Indels 35; Gaps 3;
Qy 1 QIQLVQSGGELVKPGASVRVSCASG-----YGFVWROSPGKGLWEI----- 43
Db 1 QVQLVQSGAEVKPGSSVKVSCASGTFSSYVAISWVRQAPGQGLEWMGGIIFPGTANY 60
Qy 44 -----GKATLTVDKSTSTAYMESSLRSEDTAVYFCAR-----WGQGTITVTV 85
Db 61 AQKPGQRTITADESTSTAYMESSLRSEDTAVYCARVNPFLFFAVGMDVWGQGTITVTV 120
Qy 86 SS 87
Db 121 SS 122
RESULT 14
MHMS18
Ig heavy chain precursor V region (B1-8) - mouse
N:Contains: Ig heavy chain precursor V region 186-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C:Accession: A90809; B90809; A22769; A02034; A02036
R:Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, I.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: so
A:Reference number: A90809; MUID:81234548; PMID:6788376
A:Accession: A90809
A:Molecule type: DNA
A:Residues: 1-139 <B18>
A:Cross-references: GB:J00529; NID:G195114; PIDN:AAA38170.1; PID:G195115
A:Accession: B90809
A:Molecule type: DNA
A:Residues: 1-117 <1862>
A:Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hap
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Seyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: A22769
A:Molecule type: protein
A:Residues: 20-139 <D11>
A:Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch var
of the mu chain
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status Predicted <SIG>
F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>
F:34-117/Domain: immunoglobulin homology <IMW>
F:118-124/Region: D segment
F:125-139/Region: J segment (JH2)
Query Match 74.9%; Score 335.5; DB 1; Length 139;
Best Local Similarity 58.3%; Pred. No. 6e-26;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
Qy 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVROSPGKGLWEI----- 44
Db 1 QIQLVQSGGELVKPGASVRVSCASGYST-----WVROSPGKGLWEI----- 44

Db 20 QVQLQQPGAEIVKPGASVKLSCKASGYTFISYMHVWKQRPGRGLEWIGRIDPNSGGTKY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 87
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARYDYIGSSYFDYWGQGTITVTVSS 139

RESULT 15

PC4402
pElB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein -
C:Species: synthetic
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C:Accession: PC4402
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A:Title: Construction, bacterial expression, and characterization of hapten-specific sin
A:Reference number: PC4402
A:Accession: PC4402
A:Molecule type: DNA
A:Residues: 1-287 <SUZ>
C:Keywords: fusion protein

Query Match 74.9%; Score 335.5; DB 4; Length 287;
Best Local Similarity 58.3%; Pred. No. 1.2e-25;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
QY 1 QIQLVQSGGELVKPGASVTVSCSKASGYST-----WVRQSPGKGLEWIG-----44
Db 160 QVQLQQPGAEIVKPGASVKLSCKASGYTFISYMHVWKQRPGRGLEWIGRIDPNSGGTKY 219
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 87
Db 220 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARYDYIGSSYFDYWGQGTITVTVSS 279

Search completed: January 13, 2004, 12:44:40
Job time : 7.30655 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 3.79913 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGLVKPGASRV.....DTAVVFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	335.5	74.9	139	1	HV07_MOUSE
2	329.5	73.5	137	1	HV11_MOUSE
3	329.5	73.4	117	1	HV12_MOUSE
4	329.5	73.4	117	1	HV13_MOUSE
5	322.5	72.0	118	1	HV51_MOUSE
6	319.5	71.2	120	1	HV03_MOUSE
7	318.5	71.1	120	1	HV50_MOUSE
8	315.5	70.3	140	1	HV02_MOUSE
9	311.5	69.4	138	1	HV48_MOUSE
10	305.5	68.1	121	1	HV01_MOUSE
11	302.5	67.5	147	1	HV1C_HUMAN
12	293.5	65.4	117	1	HV05_MOUSE
13	293.5	65.4	117	1	HV14_MOUSE
14	292.5	65.2	117	1	HV06_MOUSE
15	292.5	65.2	117	1	HV1B_HUMAN
16	292.5	65.2	117	1	HV52_MOUSE
17	289.5	64.5	117	1	HV09_MOUSE
18	289.5	64.5	136	1	HV15_MOUSE
19	287.5	64.1	117	1	HV04_MOUSE
20	286.5	64.0	114	1	HV3B_HUMAN
21	286.5	63.8	117	1	HV49_MOUSE
22	285.5	63.7	114	1	HV00_MOUSE
23	285.5	63.6	117	1	HV10_MOUSE
24	285.5	63.6	117	1	HV1A_HUMAN
25	281.5	62.7	119	1	HV3I_HUMAN
26	280.5	62.6	116	1	HV3T_HUMAN
27	280.5	62.6	124	1	HV1D_HUMAN
28	279.5	62.3	117	1	HV1G_HUMAN
29	279.5	62.3	121	1	HV3J_HUMAN
30	278.5	62.2	122	1	HV3G_HUMAN
31	276.5	61.7	122	1	HV3H_HUMAN
32	271.5	60.6	122	1	HV3A_HUMAN
33	271.5	60.6	126	1	HV3K_HUMAN

34	269.5	60.2	119	1	HV38_MOUSE
35	267.5	59.7	124	1	HV1E_HUMAN
36	267.5	59.6	115	1	HV3F_HUMAN
37	267.5	59.6	125	1	HV1F_HUMAN
38	266.5	59.5	119	1	HV37_MOUSE
39	266.5	59.0	136	1	HV16_MOUSE
40	263.5	58.8	114	1	HV01_CANFA
41	263.5	58.7	117	1	HV41_MOUSE
42	262.5	58.6	119	1	HV40_MOUSE
43	261.5	58.4	120	1	HV1H_HUMAN
44	261.5	58.3	142	1	HV01_RAT
45	260.5	58.1	122	1	HV21_MOUSE

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; J00529; AAA38170.1; -.
CC PIR; A30809; MMS318.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003006; IG_MHC.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; IG; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Immunoglobulin V region; Signal; 3D-structure.
CC SIGNAL
CC 1 19
CC CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DOMAIN 118 124 D SEGMENT.
CC DOMAIN 125 139 JH2 SEGMENT.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 139 139
CC SEQUENCE 139 AA; 15415 MW; 1857DD4FDC9F465 CRC64;

```

Query Match      74.9%; Score 335.5; DB 1; Length 139;
Best Local Similarity 58.3%; Pred. No. 2e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 44
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQPGAEFVXPGASVKLSCKASGYTFTSYLHMHWVQKPGKLEWIGRIDPNSGGTTY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 45 -----KATLTVDKSTAYMELSSLRSEDATAYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVQLQPGAEFVXPGASVKLSCKASGYTFTSYLHMHWVQKPGKLEWIGRIDPNSGGTTY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 45 -----KATLTVDKSTAYMELSSLRSEDATAYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLTSEDSAVVYCARYLGRFYDWFGQGTITVTVSS 137
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 943 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -|- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match      73.5%; Score 329.5; DB 1; Length 137;
Best Local Similarity 57.6%; Pred. No. 9.5e-31;
Matches 68; Conservative 11; Mismatches 8; Indels 31; Gaps 3;

```

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QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 44
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Db 20 QVQLQPGAEFVXPGASVKLSCKASGYTFTSYLHMHWVQKPGKLEWIGRIDPNSGGTTY 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 45 -----KATLTVDKSTAYMELSSLRSEDATAYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLTSEDSAVVYCARYLGRFYDWFGQGTITVTVSS 137
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
HV12 MOUSE
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -|- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -|- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE43B447B41 CRC64;

Query Match      73.4%; Score 329; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 9e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIOLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKLEWIG----- 43
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWKVKQSHGKSLWIGDINPNNGGTSY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 44 -----GKATLTVDKSTAYMELSSLRSEDATAYFCAR-----WGQGTITVTVSS 87
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKRATLTVDKSSSTAYMQLNSLTSEDSAVVYCARDYDWYFDVWGAGTITVTVSS 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
HV13 MOUSE
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN SEQUENCE.
RP MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MEMSJS.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292EAF4BE447E41 CRC64;

Query Match 73.4%; Score 329; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 9e-31;
Matches 70; Conservative 11; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIQVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 EVQLQSQPELVKPGASVRVSCKASGYFTDYNNWVKQSHGKSLWIGDINPNNGTSTY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVFCAR-----WGQGTITVTVSS 87
DB 61 NQKPKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCYCARDYVYFDVWVGAGTITVTVSS 117

RESULT 5
HV51 MOUSE
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104 V SEGMENT.
FT DOMAIN 105 118 D SEGMENT.
FT DISULFID 22 96
FT NON TER 118 118 J SEGMENT.
FT NON TER 118 118 BY SIMILARITY.
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

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Query Match 72.0%; Score 322.5; DB 1; Length 118;
Best Local Similarity 58.5%; Pred. No. 5.1e-30;
Matches 69; Conservative 9; Mismatches 9; Indels 31; Gaps 3;

QY 1 QIQVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 EVQLQSQPELVKPGASVRVSCKASGYFTDYNNWVKQSHGKSLWIGDINPNNGTSTY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVFCAR-----WGQGTITVTVSS 87
DB 61 NQKPKGKATLTVDKSSSTAYMELSLTSEDSAVYCYARGYDVPDVGTVGTTVTVSS 118

RESULT 6
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geller M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsonate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111
FT NON TER 120 120 IG-LIKE.
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 71.2%; Score 319; DB 1; Length 120;
Best Local Similarity 55.8%; Pred. No. 1.3e-29;
Matches 67; Conservative 12; Mismatches 7; Indels 34; Gaps 3;

QY 2 IQLVQSGGELVKPGASVRVSCKASGYFT-----WVRSQPGKGLEW----- 43
DB 1 VQLQSGGAEIVRAGSVKMSCKASGYFTSYGINVVKORPGQGLEWIGYINPGNGYTKYN 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVFCAR-----WGQGTITVTVSS 87
DB 61 EKFEPKGTTLTVDKSSSTAYMQLNSLTSEDSAVYFCARSVYGGSYFDVWVGQGTITVTVSS 120

RESULT 7
HV50 MOUSE
ID HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL ENBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105
FT DOMAIN 106 120
FT DISULFID 22 96
FT NON_TER 120 120
FT SEQUENCE 120 AA; 13311 MW; 914453P426F09834 CRC64;

Query Match
Best Local Similarity 71.1%; Score 318.5; DB 1; Length 120;
Matches 67; Conservative 11; Mismatches 9; Indels 33; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 44
DB 1 QVQLQPGTGLVKPGASVNLCKASGYTFTSYVMHWIRORPGGLEWIGINPSNGGNY 60
QY 45 -----KATLTVDKSTAYMELSSRSBDTAYFCAR-----WGQGTITVTVSS 87
DB 61 NEKFKGKTLTVDKSSSATYMQLSLTSDSAVYFCARVDYGDYFDVWGQGTITVTVSS 120

RESULT 8
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1978).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140
FT DOMAIN 20 139
FT NON_TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match
Best Local Similarity 70.3%; Score 315; DB 1; Length 140;
Matches 66; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 43
DB 20 EVQLQSGGAEIVRAGSVVMKSCASGYTFTSYGVNWKQRPQGLEWIGVYNGVINY 79
QY 44 -----GKATLTVDKSTAYMELSSRSBDTAYFCAR-----WGQGTITVTVSS 86
DB 80 NEKFKGKTLTVDKSSSATYMQLSLTSDSAVYFCARSHYGGSYDFDYWGQGTITVTVSS 139
QY 87 S 87
DB 140 S 140

RESULT 9
HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.P.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMS7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON_TER 138 138
FT SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match
Best Local Similarity 69.4%; Score 311; DB 1; Length 138;
Matches 66; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

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Best Local Similarity 55.5%; Pred. No. 1.3e-28;
Matches 66; Conservative 12; Mismatches 9; Indels 32; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----44
DB 20 QVQLQQSGAEELVKPGASVQLSKASGHTFTNYIHWYKQRPQGQGLEWIGINFDGDSNY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSEDSTAVYFCAR-----WGQGTIVTVSS 87
DB 80 NEKPKKATLTVDKSSSTAYMQLSSLTPSEFVAVYCARSDGYDWFVYWGQGLTVFSA 138

RESULT 10
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GVMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227ABF3EC56ED0BF CRC64;

Query Match 68.1%; Score 305; DB 1; Length 121;
Best Local Similarity 52.1%; Pred. No. 5.3e-28;
Matches 63; Conservative 14; Mismatches 10; Indels 34; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----43
DB 1 EAQVQSGAEELVKPGASVQLSKASGHTFTNYIHWYKQRPQGQGLEWIGIYPGGFTNY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDSTAVYFCAR-----WGQGTIVTVSS 86
DB 61 NDNLKQKATLTADTSSSTAYIQLSSLTSEDSALYHCARGIYNSSPYFDSWGQGTILTVS 120
QY 87 S 87
DB 121 S 121

RESULT 11
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT CHAIN 1 19
FT DOMAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 IG-LIKE.
FT DISULFID 41 115 PYRROLIDONE CARBOXYLIC ACID.
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F972A5366C20 CRC64;

Query Match 67.5%; Score 302.5; DB 1; Length 147;
Best Local Similarity 50.0%; Pred. No. 1.3e-27;
Matches 64; Conservative 13; Mismatches 10; Indels 41; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG-----43
DB 20 QIQLVQSGAEELVKPGASVRVSKASGYSTFTSYIHWYKQRPQGQGLEWIGINPNSGCTNY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDSTAVYFCAR-----WGQ 79
DB 80 APRFGQRTVMTDAGSTAYMDLRSLRSDSDSAVFYCAKSDPFWSDYNYFDYSYTLDDWGQ 139
QY 80 GTTVTVSS 87
DB 140 GTTVTVSS 147

RESULT 12
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 3 precursor.
OX IGH-VJ558.
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OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
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CC -----
CC EMBL; J00488; AAA38519.1; -
CC PIR; A02041; HVMS8A.
CC HSP; P01810; 2PB.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Igh-like.
CC InterPro; IPR003006; Igh_MHC.
CC InterPro; IPR003596; Igh_V.
CC Pfam; PF00047; Igh; 1.
CC SMART; SM00406; Igh; 1.
CC PROSITE; PS50835; IGH LIKE; 1.
CC Immunoglobulin V region; Signal.
KW CHAIN 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 65.4%; Score 293; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 1.2e-26;
Matches 59; Conservative 12; Mismatches 5; Indels 22; Gaps 2;

QY 1 QIQLVQSGGELVKPGASVRYSCKASGYFT-----WYRQSPGKLEWIG----- 44
DB 20 QVQLQPGALVRPGSSVYKLSCKASGYFTSYMDWVKRPGQGLEWIGNIYPSDSETHY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSEDSTAVYFCAR 76
DB 80 NQKFKSKATLTVDKSSSTAYMELSLRSEDSTAVYFCAR 117

RESULT 13
HV14 MOUSE
ID HV14 MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Igh heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RA "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00488; AAA38519.1; -
CC PIR; A02041; HVMS8A.
CC HSP; P01810; 2PB.
CC MGD; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Igh-like.
CC InterPro; IPR003006; Igh_MHC.
CC InterPro; IPR003596; Igh_V.
CC Pfam; PF00047; Igh; 1.
CC SMART; SM00406; Igh; 1.
CC PROSITE; PS50835; IGH LIKE; 1.
CC Immunoglobulin V region; Signal.
KW CHAIN 1
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 65.4%; Score 293; DB 1; Length 117;
Best Local Similarity 62.2%; Pred. No. 1.2e-26;
Matches 61; Conservative 9; Mismatches 6; Indels 22; Gaps 2;

QY 1 QIQLVQSGGELVKPGASVRYSCKASGYFT-----WYRQSPGKLEWIG----- 44
DB 20 EVQLQQSGPELVKPGASVKISCKASGYFTFDYMHVWKQSHGKSLWIGYIYPNGGTG 79
QY 45 -----KATLTVDKSTSTAYMELSLRSEDSTAVYFCAR 76
DB 80 NQKFKSKATLTVDKSSSTAYMELSLRSEDSTAVYFCAR 117

RESULT 14
HV06 MOUSE
ID HV06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Igh heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
CC PIR; A02032; HVMS02.
CC HSP; P01810; 2PB.
CC InterPro; IPR007110; Igh-like.
CC InterPro; IPR003006; Igh_MHC.
CC InterPro; IPR003596; Igh_V.

```

```
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCASC CRC64;

Query Match 65.2%; Score 292; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 1.6e-26;
Matches 60; Conservative 9; Mismatches 5; Indels 22; Gaps 2;

QY 2 IQLVQSGGELVKPGASVRSCKASGYSTFT-----WVRQSPGKGLEWT----- 43
Db 21 VQLQPGAGELVKPGASVRSCKASGYSTFTSYMHWKVRQPGQGLEWIGRIHPDSDTN 80
QY 44 ----GKATLTVDKSTSTAYMELSLRSEDVAVYFCA 75
Db 81 QKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYICA 116

RESULT 15
HVLB HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00240; AAB52988.1; -.
DR PIR; A02024; HVHUG.
DR HSP; F01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
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FT NON TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 65.2%; Score 292; DB 1; Length 117;
Best Local Similarity 60.2%; Pred. No. 1.6e-26;
Matches 59; Conservative 10; Mismatches 7; Indels 22; Gaps 2;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFT-----WVRQSPGKGLEWT----- 43
Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYMHVWRQAPGQGLEWMGIINPSSGGSYSY 79
QY 44 ----GKATLTVDKSTSTAYMELSLRSEDVAVYFCA 76
Db 80 AOKFQGRVIMTRDTSTIVMELSLRSEDVAVYCAR 117

Search completed: January 13, 2004, 12:39:26
Job time : 4.79913 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 15.5764 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-90
Perfect score: 448
Sequence: 1 QIQLVQSGELVPGASRV.....DTAVFCARWGQTTTVSS 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp:archaea:*
- 2: sp:bacteria:*
- 3: sp:fungi:*
- 4: sp:human:*
- 5: sp:invertebrate:*
- 6: sp:mammal:*
- 7: sp:mhc:*
- 8: sp:organelle:*
- 9: sp:phage:*
- 10: sp:plant:*
- 11: sp:rodent:*
- 12: sp:virus:*
- 13: sp:vertebrate:*
- 14: sp:unclassified:*
- 15: sp:virus:*
- 16: sp:bacteriap:*
- 17: sp:archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340	75.9	473	11 Q9D8L4	Q9d8l4 mus musculus
2	339.5	75.8	137	11 Q924R6	Q924r6 mus musculus
3	338	75.4	142	11 Q924Q1	Q924q1 mus musculus
4	337.5	75.3	141	11 Q924Q4	Q924q4 mus musculus
5	337	75.2	140	11 Q924R2	Q924r2 mus musculus
6	335.5	74.9	143	11 Q924R0	Q924r0 mus musculus
7	335.5	74.9	145	11 Q924Q7	Q924q7 mus musculus
8	335	74.8	146	11 Q924R8	Q924r8 mus musculus
9	335	74.8	146	11 Q924Q6	Q924q6 mus musculus
10	334.5	74.7	145	11 Q924Q9	Q924q9 mus musculus
11	334.5	74.7	145	11 Q924R1	Q924r1 mus musculus
12	334.5	74.7	145	11 Q924R4	Q924r4 mus musculus
13	334.5	74.6	146	11 Q924Q3	Q924q3 mus musculus
14	334	74.6	146	11 Q924Q5	Q924q5 mus musculus
15	333.5	74.4	143	11 Q924Q3	Q924q3 mus musculus
16	332.5	74.2	145	11 Q924R3	Q924r3 mus musculus

17	332	74.1	117	11 Q9QXP0	Q9qxf0 mus musculus
18	331.5	74.0	482	11 Q8K172	Q8k172 mus musculus
19	331	73.9	117	11 Q9QXE9	Q9qxe9 mus musculus
20	330.5	73.8	143	11 Q924R7	Q924r7 mus musculus
21	329	73.4	119	5 Q9GYZ2	Q9gyz2 schistosoma
22	328.5	73.3	143	11 Q924Q0	Q924q0 mus musculus
23	328.5	73.3	145	11 Q924P7	Q924p7 mus musculus
24	328	73.2	481	11 Q91WT1	Q91wt1 mus musculus
25	327.5	73.1	143	11 Q924Q9	Q924q9 mus musculus
26	327	73.0	142	11 Q924Q2	Q924q2 mus musculus
27	327	73.0	144	11 Q924P5	Q924p5 mus musculus
28	325.5	72.7	143	11 Q91VA2	Q91va2 mus musculus
29	325	72.5	140	11 Q924P8	Q924p8 mus musculus
30	324.5	72.4	143	11 Q924P6	Q924p6 mus musculus
31	323	72.1	119	4 Q8UL94	Q8ul94 homo sapien
32	323	72.1	123	11 Q8V1D1	Q8v1d1 mus musculus
33	323	72.1	147	11 Q925S3	Q925s3 mus musculus
34	322.5	72.0	124	4 Q8UL92	Q8ul92 homo sapien
35	322.5	72.0	139	11 Q924R5	Q924r5 mus musculus
36	322.5	72.0	463	11 Q99LC4	Q99lc4 mus musculus
37	320.5	71.5	159	4 Q96QS0	Q96qs0 homo sapien
38	318.5	71.1	118	11 Q9Z1C4	Q9z1c4 mus musculus
39	317.5	70.9	143	11 Q91V67	Q91v67 mus musculus
40	316	70.5	474	11 Q8R3H6	Q8r3h6 mus musculus
41	315.5	70.4	488	11 Q8K0F2	Q8k0f2 mus musculus
42	315.5	70.4	500	4 Q8BRV0	Q8brv0 homo sapien
43	315.5	70.4	613	11 Q8VCX7	Q8vcx7 mus musculus
44	314.5	70.2	278	11 Q921K1	Q921k1 mus musculus
45	314	70.1	120	11 Q920E8	Q920e8 mus musculus

ALIGNMENTS

RESULT 1

Q9D8L4	PRELIMINARY;	PRT;	473 AA.
ID Q9D8L4			
AC Q9D8L4			
DT 01-JUN-2001 (TREMBLrel. 17, Created)			
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DB 1810060009Rik protein.			
GN IGH-1 OR 1810060009Rik.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C57BL/6J; TISSUE=Pancreas;			
RX MEDLINE=21085650; PubMed=11217851;			
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Cavaant T.,			
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,			
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,			
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,			
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,			
RA Hayashizaki Y.			
RT *Functional annotation of a full-length mouse cDNA collection.*;			
RL Nature 409:685-690(2001).			
EMBL; AK007918; BAB25349.1;			
DR HSSP; P01842; 7FAB.			

01-WAR-2003 (TRENBLrel. 23, Last annotation update)
V23-D-J-C mu protein (fragment).
V23-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069913; BAB63291.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
Query Match 75.4%; Score 338; DB 11; Length 142;
Best Local Similarity 60.7%; Pred. No. 4.4e-30;
Matches 71; Conservative 11; Mismatches 5; Indels 30; Gaps 3;
3;
QY 1 QTLVQSGGELVPGASRVSCASGYST----WVROSPKGLEWIG----- 44
Db 1 QVQLQQPTGLVPGASVKLSKASGYTTSYMHVWKQRPQGGLIEWINPNSGTTY 60
QY 45 -----KATLVDSKSTAYWELSSRSDDTAVYFCAR-----WGQGTIVTVSS 87
Db 61 NEKFSKATLVDSKSSSTAYWELSSRSDDTAVYFCAR-----WGQGTIVTVSS 117
117
RESULT 4
Q924Q4
ID Q924Q4 PRELIMINARY; PRT; 141 AA.
AC Q924Q4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-WAR-2003 (TRENBLrel. 23, Last annotation update)
DE V186. 2-D-J-C mu protein (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067796; BAB63281.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 141 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;
Query Match 75.3%; Score 337.5; DB 11; Length 141;
Best Local Similarity 60.3%; Pred. No. 4.9e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;
3;

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QY 1 QIQLVQSGGELVKPGASVVRVSKASGYST-----WVQSPGKGLWIG----- 44
DR EMBL; AB067793; BAB63275.1;
DB 1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
QY 45 -----KATLVTDKSTSTAYMELSSLSRSEDYAVYFCAR-----WQGGTTVTSS 87
DR SMART; SM00406; IGV; 1.
DB 61 NEKPKSKATLVTDKPSSTAYMQLSLSLTSSEDSAVYVCARYDYGGSYFDYWGQGTTLTVSS 116
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

RESULT 5
Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067788; BAB63273.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 140
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 75.2%; Score 337; DB 11; Length 140;
Best Local Similarity 60.9%; Pred. No. 5.5e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 28; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVVRVSKASGYST-----WVQSPGKGLWIG----- 44
DB 1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLVTDKSTSTAYMELSSLSRSEDYAVYFCAR-----WQGGTTVTSS 87
DB 61 NEKPKSKATLVTDKPSSTAYMQLSLSLTSSEDSAVYVCARYDYGGSYFDYWGQGTTLTVSS 115
FT NON_TER 140
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

RESULT 6
Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 74.9%; Score 335.5; DB 11; Length 145;
Best Local Similarity 58.3%; Pred. No. 8.5e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVVRVSKASGYST-----WVQSPGKGLWIG----- 44
DB 1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLVTDKSTSTAYMELSSLSRSEDYAVYFCAR-----WQGGTTVTSS 87
DB 61 NEKPKSKATLVTDKPSSTAYMQLSLSLTSSEDSAVYVCARYDYGGSYFDYWGQGTTLTVSS 120
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

RESULT 8
Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 146
FT NON_TER 146
SQ SEQUENCE 146 AA; 16141 MW; 55A59A7908B2CD6A CRC64;
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RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 74.9%; Score 335.5; DB 11; Length 143;
Best Local Similarity 59.3%; Pred. No. 8.4e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 31; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVVRVSKASGYST-----WVQSPGKGLWIG----- 44
DB 1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLVTDKSTSTAYMELSSLSRSEDYAVYFCAR-----WQGGTTVTSS 87
DB 61 NEKPKSKATLVTDKPSSTAYMQLSLSLTSSEDSAVYVCARYDYGGSYFDYWGQGTTLTVSS 118
FT NON_TER 143
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

RESULT 7
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AC Q924Q7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 74.9%; Score 335.5; DB 11; Length 145;
Best Local Similarity 58.3%; Pred. No. 8.5e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVVRVSKASGYST-----WVQSPGKGLWIG----- 44
DB 1 QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLVTDKSTSTAYMELSSLSRSEDYAVYFCAR-----WQGGTTVTSS 87
DB 61 NEKPKSKATLVTDKPSSTAYMQLSLSLTSSEDSAVYVCARYDYGGSYFDYWGQGTTLTVSS 120
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

RESULT 8
Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16216 MW; 92460FDF1B7538 CRC64;

Query Match 74.8%; Score 335; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 9.8e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTVS 86
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYAMDYWGQGTITVTVS 120

QY 87 S 87
DB 121 S 121

RESULT 9
Q924Q8 PRELIMINARY; PRT; 146 AA.
ID Q924Q8
AC Q924Q8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067792; BAB63277.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
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SQ SEQUENCE 146 AA; 16023 MW; 4B04959991D49159 CRC64;

Query Match 74.8%; Score 335; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 9.8e-30;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTVS 86
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYAMDYWGQGTITVTVS 120

QY 87 S 87
DB 121 S 121

RESULT 10
Q924Q6 PRELIMINARY; PRT; 145 AA.
ID Q924Q6
AC Q924Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067794; BAB63279.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
Best Local Similarity 58.3%; Pred. No. 1.1e-29;
Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYST-----WVRQSPGKLEWIG----- 44
DB 1 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSSEDTAVYFCAR-----WGQGTITVTVS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYAMDYWGQGTITVTVS 120

RESULT 11
Q924Q9 PRELIMINARY; PRT; 145 AA.
ID Q924Q9
AC Q924Q9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE VHI86.2-D-J-C mu protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067791; BAB63276.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44
 DB 1 QVQLQPGAEVLVPGASVKLSCKASGYFTFTSYMHWYKQRPGRGLEWIGRIDPNSGGTKY 60
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCARVDGSSPYAMDYWGQGTSTVTVSS 120

RESULT 12
 Q924R1 PRELIMINARY; PRT; 145 AA.
 AC Q924R1
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vh186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067789; BAB63274.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44
 DB 1 QVQLQPGAEVLVPGASVKLSCKASGYFTFTSYMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

RESULT 13
 Q924R4 PRELIMINARY; PRT; 145 AA.
 AC Q924R4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vh186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067797; BAB63282.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16081 MW; ECDBLA135E05B8AA CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44
 DB 1 QVQLQPGAEVLVPGASVKLSCKASGYFTFTSYMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCARVDGSSPYAMDYWGQGTSTVTVSS 120

RESULT 13
 Q924R4 PRELIMINARY; PRT; 145 AA.
 AC Q924R4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vh186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067785; BAB63270.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16081 MW; ECDBLA135E05B8AA CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44
 DB 1 QVQLQPGAEVLVPGASVKLSCKASGYFTFTSYMHWYKQRPGRGLEWIGRIDPNSGGTKY 60
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVVYCARVDYDYAMDYWGQGTSTVTVSS 120

RESULT 14
 Q924Q3 PRELIMINARY; PRT; 146 AA.
 AC Q924Q3
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Vh186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067797; BAB63282.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR NON_TER 1
 FT NON_TER 146
 SQ SEQUENCE 146 AA; 16081 MW; ECDBLA135E05B8AA CRC64;

Query Match 74.7%; Score 334.5; DB 11; Length 145;
 Best Local Similarity 58.3%; Pred. No. 1.1e-29;
 Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGELVPGASVRVSCKASGYFT-----WVRSQPGKLEWIG----- 44
 DB 1 QVQLQPGAEVLVPGASVKLSCKASGYFTFTSYMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

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DR pfam; PF00047; ig; 1.
DR SMART; SM00406; igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEASDD6EL955807F CRC64;

Query Match      74.4%; Score 334; DB 11; Length 146;
Best Local Similarity 57.9%; Pred. No. 1.3e-29;
Matches 70; Conservative 11; Mismatches 6; Indels 34; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSCKASGYST-----WVRSFGKGLEWIG----- 44
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQPGAGELVKPGASVKLSCKASGYTFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDSTAVYFCAR-----WQQGTTVTVS 86
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARSLYDYGDIYDYGQTSVTVS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 87 S 87
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Db 121 S 121

RESULT 15
Q924Q5 PRELIMINARY; PRT; 143 AA.
AC Q924Q5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067795; BAB63280.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match      74.4%; Score 333.5; DB 11; Length 143;
Best Local Similarity 59.3%; Pred. No. 1.4e-29;
Matches 70; Conservative 10; Mismatches 7; Indels 31; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSCKASGYST-----WVRSFGKGLEWIG----- 44
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Db 1 QVQLQPGAGELVKPGASVKLSCKASGYTFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDSTAVYFCAR-----WQQGTTVTVS 87
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYICARFYDYEDYDYGQTSVTVS 118
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Search completed: January 13, 2004, 12:43:06
Job time : 16.5764 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 20.2873 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASRV.....DTAVFYCARWGQGTWTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	370	82.6	87	ABG74721	Murine humanised M
3	367	81.9	115	AA121218	Humanised HBV pre-
4	366	81.7	177	AA933003	Homologous sequenc
5	365	81.5	117	AAW84037	Humanised anti-alp
6	360.5	80.5	135	AA107965	A heavy chain vari
7	360	80.4	136	AAW06442	HuMc3 VH region.
8	356	79.5	121	AA928744	Heavy chain variab
9	356	79.5	136	AA171548	Humanised antibody

10	354	79.0	470	21	AAW90935	Humanised anti-Fas
11	354	79.0	470	23	ABG74904	Mouse humanised an
12	353.5	78.9	116	17	AA92218	Humanised LL2 MAB
13	353.5	78.9	116	18	AAW27698	Variable heavy cha
14	353.5	78.9	135	13	AA929017	pUC-RVh-1220d. Sy
15	353.5	78.9	139	19	AAW65773	Anti-human HMI.24
16	353.5	78.9	139	19	AAW65774	Anti-human HMI.24
17	353.5	78.9	139	19	AAW62205	Humanised anti-HMI
18	353.5	78.9	139	19	AAW62206	Humanised anti-HMI
19	353.5	78.9	139	20	AAW32770	Anti-HMI.24 antibo
20	353.5	78.9	139	20	AAW32771	Anti-HMI.24 antibo
21	353.5	78.9	139	20	AAW02575	Humanised H chain
22	353.5	78.9	139	20	AAW02572	Humanised H chain
23	353.5	78.9	139	20	AAW05486	H chain V region c
24	353.5	78.9	139	20	AAW05487	H chain V region c
25	353.5	78.9	139	23	AAW52354	H chain V region v
26	353.5	78.9	139	23	AAW52355	H chain V region v
27	353.5	78.9	139	24	ABG71946	Human reshaped ant
28	353.5	78.9	140	19	AAW77294	HMI.24 antibody he
29	352.5	78.7	115	18	AAW22418	Reshaped human AUK
30	352.5	78.7	135	13	AAW29016	PUC-RVh-1220b. Sy
31	352.5	78.7	139	19	AAW62212	Humanised anti-HMI
32	352.5	78.7	139	20	AAW02564	Humanised H chain
33	352.5	78.7	139	20	AAW02558	Humanised H chain
34	352.5	78.7	448	23	AAW49203	Humanised monoclon
35	351	78.3	121	23	AAE27819	Mouse 425 antibody
36	351	78.3	121	23	ABG32691	Murine anti-EGPR a
37	351	78.3	470	21	AAW50933	Humanised anti-Fas
38	351	78.3	470	23	ABW74902	Humanised anti-Fas
39	350.5	78.2	116	14	AAW38617	Modified (prop) he
40	350.5	78.2	116	19	AAW58510	Protein SEQ ID NO:
41	350	78.1	119	19	AAW49813	Amino acid sequenc
42	350	78.1	222	14	AAW39267	Humanised C4G1 Ig
43	350	78.1	222	19	AAW49817	Fragment of humani
44	350	78.1	235	14	AAW39268	Humanised C4G1 Ig
45	350	78.1	235	19	AAW49818	Amino acid sequenc

ALIGNMENTS

RESULT 1
AA92991
ID AA92991 standard; Protein; 87 AA.

AC AA92991;

XX (updated)

DT 25-MAR-2003

DT 18-MAY-1996 (first entry)

DE Homologous sequences to antibody IOR-R3 variable region heavy chain.

XX IOR-R3; monoclonal antibody; human; mouse; heavy chain; homology;

XX variable region; epidermal growth factor receptor; hybridoma;

XX framework; cloning; computer; algorithm; immunogenicity;

XX site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;

XX point mutation; antibody engineering; protein engineering;

XX humanised antibody; antitumour; cancer; therapy.

OS Homo sapiens.

XX Location/Qualifiers

FT 26..30

FT /note= "Amino acids involved in tertiary structure"

FT 76

FT /note= "Amino acid involved in tertiary structure"

XX EP699755-A2.

XX 06-MAR-1996.

XX 27-JUN-1995; 95EP-0201752.

XX

PR 30-JUN-1994; 94CU-000080.
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
PA Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX WPI; 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig
PT T-cell epitopes - by sequence comparison, also humanised antibodies
PT confg. altered T-cell epitopes, retaining antigen specificity but
PT not immunogenicity, esp. for tumour treatment
XX
XX Claim 14; Fig 2; 33pp; English.
XX
XX The sequence represents residues from a human immunoglobulin with
CC homology to the heavy chain variable region from monoclonal antibody
CC IOR-R3 (AAR92990), specific for epidermal growth factor receptor,
CC produced by a mouse hybridoma. The sequence is partial, and
CC complementarity determining regions are omitted. The sequence is
CC isolated by comparison of human and mouse immunoglobulins and
CC analysis for T-lymphocyte antigenic sequences using a computer
CC algorithm. Residues not within a complementarity determining region,
CC canonical structure or Vennier zone may be modified to reduce
CC immunogenicity in humans (e.g. in sequence AAR92992). This method,
CC which involves the introduction of only a few point mutations into
CC T-cell epitope coding regions, is generally applicable in humanisation
CC of mouse antibodies. The resulting humanised antibodies may be used
CC e.g. as antitumour agents. They retain the antigen recognition of the
CC original antibody, but are not immunogenic in humans.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 87 AA;
SQ

Query Match 83.9%; Score 376; DB 17; Length 87;
Best Local Similarity 79.3%; Pred. No. 4.3e-28;
Matches 69; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFTVVRQSPGKLEWIGKATLTVDKSTSTAYME 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYSTFTNVRQAPGQGLEWVGRTVTRTSTSTAYME 60
QY 61 LSSLRSEDVAVYFCARWGQGLTVTVSS 87
Db 61 LSSLRSEDVAVYFCARWGQGLTVTVSS 87
RESULT 2
ABG74721
ID ABG74721 standard; Protein; 87 AA.
XX
XX ABG74721;
XX
XX 10-MAY-2003 (first entry)
XX Murine humanised Mu007-associated protein DP-5.
XX
XX Murine; light chain; variable region; antibody; Crohn's disease;
XX human interleukin (IL)-beta; antiarthritic; antiarthritic; humanised;
XX antiinflammatory; osteopathic; antiallergic; cerebroprotective;
XX antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;
XX rheumatoid arthritis; osteoarthritis; cartilage destruction;
XX allergy; septic shock; endotoxemia; stroke; asthma;
XX graft versus host disease; inflammatory bowel disease; DP-5.
XX Unidentified.
XX
XX WO2003010282-A2.
XX
XX 06-FEB-2003.
XX
XX 18-JUL-2002; 2002WO-US21281.
XX

PR 26-JUL-2001; 2001US-307973P.
PR 14-AUG-2001; 2001US-312278P.
XX
XX (ELIL) LILLY & CO ELI.
XX
XX Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N;
PI Vasquez MJ;
PI
XX WPI; 2003-248068/24.
XX
XX New IL-beta antibodies, useful for treating allergy, septic or
PT endotoxic shock, septicemia, stroke, asthma, graft versus host disease,
PT Crohn's disease, or inflammatory bowel disease
XX
XX Disclosure; Fig 2; 98pp; English.
XX
XX This invention describes a novel antibody that specifically binds mature
CC human interleukin (IL)-beta, and binds the same epitope on mature human
CC IL-beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
CC The antibody of the invention have antirheumatic, antiarthritic,
CC antiinflammatory, osteopathic, antiallergic, cerebroprotective,
CC antiasthmatic, immunosuppressive and antibacterial activity and can be
CC used in a vaccine. The antibody is useful for manufacturing a medicament
CC for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
CC cartilage destruction in a subject. The antibody is also useful for
CC treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,
CC graft versus host disease, Crohn's disease, or inflammatory bowel
CC disease. This sequence represents a protein associated with the
CC humanised murine Mu007 antibody described in the disclosure of the
CC invention.
XX
XX Sequence 87 AA;
SQ

Query Match 82.6%; Score 370; DB 24; Length 87;
Best Local Similarity 78.2%; Pred. No. 1.6e-27;
Matches 68; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFTVVRQSPGKLEWIGKATLTVDKSTSTAYME 60
Db 1 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTVVRQAPGKLEWVGRTVTRTSTSTAYME 60
QY 61 LSSLRSEDVAVYFCARWGQGLTVTVSS 87
Db 61 LSSLRSEDVAVYFCARWGQGLTVTVSS 87
RESULT 3
AAB12168
ID AAB12168 standard; Protein; 115 AA.
XX
XX AAB12168;
XX
XX 17-JAN-2001 (first entry)
XX
XX Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.
XX
XX Humanised antibody; HBV surface antigen pre-S1; mouse;
XX human; hepatitis B; liver cirrhosis; liver cancer.
XX
XX Chimeric - Homo sapiens.
XX Chimeric - Mus sp.
XX
XX WO2000031141-A1.
XX
XX 02-JUN-2000.
XX
XX 19-NOV-1999; 99WO-KR00699.
XX
XX 19-NOV-1998; 98KE-0049663.
XX
XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX (GREC) KOREA GREEN CROSS CORP.
XX

```

PI Hong HJ, Ryu CJ, Hur H;
XX
XX WPI: 2000-400048/34.
XX N-PSDB; AAR62116.
XX
XX Humanized antibody specific for hepatitis B virus surface antigen
XX pre-S1, containing humanized heavy and light chain regions, useful for
XX preventing hepatitis B virus (HBV) infection and for treating chronic
XX hepatitis B.
XX
XX Claim 2; Fig 1; 61pp; English.
XX
XX Hepatitis B virus (HBV) is responsible for hepatitis infection in
XX humans, which may progress to liver cirrhosis or cancer. One of HBV's
XX surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
XX antigen may efficiently neutralise HBV. The present invention relates to
XX humanised antibodies specific for HBV surface antigen pre-S1. The
XX humanised antibodies are useful for preventing HBV infection and for
XX treating chronic hepatitis B. The Complementarity Determining Regions of
XX mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
XX the humanised antibodies of the present invention. The present sequence
XX is the humanised pre-S1 antibody HRR127HC(I) heavy chain variable region
XX (VH). The coding sequence for the present sequence was produced from the
XX coding sequence of the mouse pre-S1 antibody VH sequence (AAA62115).
XX
XX Sequence 115 AA;
SQ
Query Match 81.9%; Score 367; DB 21; Length 115;
Best Local Similarity 67.0%; Pred. No. 3.9e-27;
Matches 77; Conservative 7; Mismatches 3; Indels 28; Gaps 3;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYST-----WVRSQPGKLEWV----- 43
DB 1 QVQLVQSGAEVVKPGASVRSCKASGYAFSSSMNWRQAPGQGLEWIGRIYVPGDNTY 60
QY 44 -----QKATLVDPKSTAYMELSLRSEDYVYFCAR-----WQGGTVTVSS 87
DB 61 AQKFGKATLTADKSTAYMELSLRSEDYVYFCAREYDAYWQGGTLTVSS 115
RESULT 4
AAR93003
ID AAR93003 standard; Protein; 87 AA.
XX
XX AAR93003;
XX
XX 25-MAR-2003 (updated)
XX 18-MAY-1996 (first entry)
XX
XX Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.
XX IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology;
XX variable region; framework; cloning; computer; algorithm;
XX immunogenicity; site-directed mutagenesis; T-lymphocyte epitope;
XX tertiary structure; point mutation; antibody engineering;
XX protein engineering; humanised antibody; antitumour; cancer; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 26..30
XX /note= "Amino acid involved in tertiary structure"
XX Region 50
XX /note= "Amino acid involved in tertiary structure"
XX Region 76
XX /note= "Amino acid involved in tertiary structure"
XX
XX EP699755-A2.
XX
XX 06-MAR-1996.
XX
XX 27-JUN-1995; 95EP-0201752.
XX

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PR 30-JUN-1994; 94CU-0000080.
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
XX Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX WPI; 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig
XX T-cell epitopes - by sequence comparison, also humanised antibodies
XX contg. altered T-cell epitopes, retaining antigen specificity but
XX not immunogenicity, esp. for tumour treatment
XX
XX Claim 22; Fig 9; 33pp; English.
XX
XX The sequence represents residues from a human immunoglobulin with
XX homology to the heavy chain variable region from mouse monoclonal
XX antibody IOR-CEA-1 (AAR93002). The sequence is partial, and
XX complementarity determining regions are omitted. The sequence is
XX isolated by comparison of human and mouse immunoglobulins and
XX analysis for T-lymphocyte antigenic sequences using a computer
XX algorithm. Residues not within a complementarity determining region,
XX canonical structure or Verrier zone may be modified to reduce
XX immunogenicity in humans (e.g. in sequence AAR93004). This method,
XX which involves the introduction of only a few point mutations into
XX T-cell epitope coding regions, is generally applicable in humanisation
XX of mouse antibodies. The resulting humanised antibodies may be used
XX e.g. as antitumour agents. They retain the antigen recognition of the
XX original antibody, but are not immunogenic in humans.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 87 AA;
Query Match 81.7%; Score 366; DB 17; Length 87;
Best Local Similarity 77.0%; Pred. No. 3.7e-27;
Matches 67; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFWRSQPGKLEWIKATLVDPKSTAYME 60
DB 1 QVQLVQSGAEVVKPGASVRSCKASGYTFWRSQPGKLEWIGRVITTRDTSASTAYME 60
QY 61 LSSLRSEDYVYFCARWQGGTVTVSS 87
DB 61 LSSLRSEDYVYFCARWQGGTVTVSS 87
RESULT 5
AAR84097
ID AAR84097 standard; Protein; 117 AA.
XX
XX AAR84097;
XX
XX 15-MAR-1999 (first entry)
XX
XX Humanised anti-alpha-v beta-3 MAB D12H2HC 1-0 VH.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX angiogenesis; diabetic retinopathy; inflammation;
XX macular degeneration; osteoporosis; Paget's disease;
XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX D12H2HC-10.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /label= CDR1
XX Region 50..66
XX /label= CDR2
XX Region 99..106

```

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FT  /label= CDR3
XX  WO9840488-A1.
XX  17-SEP-1998.
XX  12-MAR-1998; 98WO-US04987.
XX  12-MAR-1997; 97US-0039609.
XX  (SMTK ) SMITHKLINE BEECHAM CORP.
XX  Johanson KO, Jonak ZL, Taylor AH;
XX  WPI; 1999-034590/03.
XX  N-PSDB; AAV71799.
XX  New anti alpha v beta_3 vitronectin receptor antibodies - used for
XX  immunotherapeutic treatment of e.g. diabetic retinopathy,
XX  inflammatory disorders, atherosclerosis, restenosis, cancers or
XX  osteoporosis
XX  Claim 1; Page 58; 97pp; English.
XX  This is the amino acid sequence of the heavy chain variable region
XX  (VH) of humanised anti-alpha-v beta-3 vitronectin receptor
XX  monoclonal antibody D12H2C 1-0. It is based on the VH sequence
XX  (see AAW84095) of human Kabat subgroup I VH, with complementarity
XX  determining regions (CDRs) from the murine anti-human alpha-v
XX  beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093).
XX  7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)
XX  are retained. The humanised heavy chain can be expressed in host
XX  cells using nucleic acid molecules (see AAV71799) of the invention.
XX  Humanised D12 VL is also provided (see AAW84098)). The humanised
XX  antibodies can be used for passive immunotherapy of disorders
XX  mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
XX  angiogenic-related disorders, such as angiogenesis associated
XX  with diabetic retinopathy, atherosclerosis and restenosis, chronic
XX  inflammatory disorders, macular degeneration, rheumatoid arthritis
XX  and cancer, e.g. solid tumour metastasis, and diseases where bone
XX  resorption is associated with pathology such as osteoporosis,
XX  hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
XX  osteolytic lesions produced by bone metastasis, bone loss due to
XX  immobilisation or sex hormone deficiency. They can also be used for
XX  targeted drug therapy, and for detection and diagnosis.
XX  SQ Sequence 117 AA;
    Query Match 81.5%; Score 365; DB 20; Length 117;
    Best Local Similarity 65.8%; Pred. NO. 6.2e-27;
    Matches 77; Conservative 7; Mismatches 3; Indels 30; Gaps 3;
    QY 1 QIQLVSGGELVKPGASVRSCKASGYST-----WVRQSPGKGLW----- 43
    DB 1 QVQLVSGAEVKKPGASVKVSCKASGYFTSYMTWRVQAPQGGLWGYDIPNGDTFF 60
    QY 44 -----GKATLTVDKSTAYMELSLRSEDITAVYFCAR-----WQGGTTVTVSS 87
    DB 61 NQKFKGKATLTVDKSTAYMELSLRSEDITAVYFCARQNYGSFYAWGQGLTVTVSS 117

RESULT 6
AAB07965
ID AAB07965 standard; Protein; 135 AA.
XX AC AAB07965;
XX 14-NOV-2000 (first entry)
XX A heavy chain variable region of humanised 3S1 antibody.
XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
XX autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
XX aplastic anaemia; myeloid dysplasia syndrome.
XX Synthetic.
XX Mus sp.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /note= "signal peptide"
XX Region 20..135
XX Region /note= "mature protein"
XX Region 50..54
XX Region /note= "complementarity determining region 1"
XX Region 69..85
XX Region /note= "complementarity determining region 2"
XX Region 118..124
XX Region /note= "complementarity determining region 3"
XX WO200047625-A2.
XX 17-AUG-2000.
XX 09-FEB-2000; 2000WO-US03303.
XX 12-FEB-1999; 99US-0249011.
XX 24-JUN-1999; 99US-0339596.
XX (CEMY ) GENETICS INST INC.
XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
XX Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX WPI; 2000-524532/47.
XX N-PSDB; AAA59694.
XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
XX from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
XX modulates immune responses and can therefore treat e.g. autoimmune
XX diseases, infectious diseases -
XX Example 3; Fig 2A; 162pp; English.
XX The present sequence represents the heavy chain variable region
XX of the humanised murine antibody 3p1. The antibody has a binding
XX specificity to B7 molecules. The antibody is used to construct humanized
XX immunoglobulins, which comprise an antigen binding region of non-human
XX origin and a portion of a human immunoglobulin. The humanized
XX immunoglobulins are useful for treating autoimmune diseases, infectious
XX diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
XX mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
XX inflammatory dermatitis, and multiple sclerosis. The immunoglobulins
XX also useful for treating a transplant recipient or preventing transplant
XX rejection in a transplant recipient, and treating proliferative disease
XX (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
XX thalassemia and aplastic anaemia), inborn errors of metabolism,
XX congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX SQ Sequence 135 AA;
    Query Match 80.5%; Score 360.5; DB 21; Length 135;
    Best Local Similarity 64.7%; Pred. NO. 1.9e-26;
    Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;
    QY 1 QIQLVSGGELVKPGASVRSCKASGYST-----WVRQSPGKGLW----- 43
    DB 20 QVQLVSGAEVKKPGASVKVSCKASGYFTFDYAIQWRQAPQGGLWGVINIVYDNTNY 79
    QY 44 -----GKATLTVDKSTAYMELSLRSEDITAVYFCAR-----WQGGTTVTVSS 87

```

Db 80 NQKFKGATMTVDKSTSTAYMELSSLRSEDTAVYCARAATMYDYGQGLTVTVSS 135

RESULT 7
AAW06442
ID AAW06442 standard; Protein; 136 AA.
AC AAW06442;
XX
XX 04-FEB-1997 (first entry)
XX
XX HuMc3 VH region.
XX
XX Humanised antibody; variable heavy region; buried residue modification;
KW VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation;
KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;
KW breast membrane glycoprotein; therapy; immunotherapy.
XX
XX Synthetic.
XX
XX WO9608565-A2.
XX
XX 21-MAR-1996.
XX
XX 14-SEP-1995; 95WO-US11683.
XX
XX 07-JUN-1995; 95US-0487598.
XX
XX 16-SEP-1994; 94US-0307868.
XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX Ceriani RI, Do Couto FJR, Peterson JA;
XX
XX WPI; 1996-179941/19.
XX
XX N-PSDB; AAT42717.
XX
XX Recombinant Mc3 antibody which binds BA46 antigen of HMFG -
PT comprises a modified heavy or light chain variable region, useful in
PT the diagnosis and therapy of breast cancer
XX
XX Claim 13; Fig 18; 91pp; English.
XX
XX This sequence represents the variable heavy (VH) chain of the humanised
CC murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the
CC buried residue modification technique, where important non-human
CC framework residues are unaffected. The Mc3 antibody binds to the BA46
CC antigen of the human milk fat globule (HMFG). The milk fat globule
CC membrane is derived from the apical surface of the mammalian epithelial
CC cell during lactation, and therefore is a source for breast membrane
CC glycoproteins. The antibody can be used in an in vitro method to detect
CC a HMFG antigen (or antigen fragment), and to diagnose the presence of the
CC antigen in a subject. The antibody can also be used to deliver an agent
CC to a target (within a subject's body), containing a HMFG antigen. The
CC antibodies can also be used for diagnosis, prognosis, and therapeutic
CC applications of breast cancer. As the humanised antibodies retain their
CC high affinity binding to the antigen, they are useful for
CC immunodiagnostic and immunotherapeutic applications in humans.
XX
XX Sequence 136 AA;
SQ
Query Match 80.4%; Score 360; DB 17; Length 136;
Best Local Similarity 65.8%; Pred. No. 2.1e-26;
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;
QY 1 QIQLVQSGGELVKGASVYVSCKASGYSTFT-----WYQSPFGKLEWIG----- 44
20 EVQLVQSGAEVKGASVYVSCKASGYSTFTGTHHWKQSPGNLEWIGLIPYNGGTY 79
Db 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
80 NQKFDKATLTVDKSTSTAYMELSSLRSEDTAVYFCARRWRYMTDYGQGLTVTVSS 136

Db 80 NQKFKGATMTVDKSTSTAYMELSSLRSEDTAVYCARAATMYDYGQGLTVTVSS 135

RESULT 8
AAR28744
ID AAR28744 standard; Protein; 121 AA.
XX
XX AAR28744;
XX
XX 25-MAR-2003 (updated)
DT 11-JAN-1993 (first entry)
XX
XX Heavy chain variable domain of GEU humanised CDR grafted Ab.
XX
XX monoclonal antibody; humanised; chimeric; CDR; neoplastic therapy;
KW shock; antilymphocyte therapy; endotoxin shock; septic shock;
KW sepsis; cardiovascular shock; tumour necrosis factor alpha;
KW multi-organ failure.
XX
XX Chimeric.
XX
XX WO9211383-A1.
XX
XX 09-JUL-1992.
XX
XX 20-DEC-1991; 91WO-GB02300.
XX
XX 21-DEC-1990; 90WO-GB02017.
PR 03-MAY-1991; 91GB-0009645.
XX
XX (CLLT) CELLTech LTD.
XX
XX Adair JR, Athwal DS, Bodmer MW, Entage JS;
XX
XX WPI; 1992-250102/30.
XX
XX Recombinant antibody specific for human TNF-alpha - for treatment
PT of shock and immuno:regulatory and inflammatory disorders, also
PT used in diagnosis
XX
XX Example 1; Fig 1; 57pp; English.
XX
XX This sequence is that of the heavy chain variable domain of a chimeric
CC antibody to an epitope of human tumour necrosis factor. It is also known
CC as hTNF1. Mouse CDRs were used at positions 26-35 (CDR1),
CC 50-65 (CDR2), and 95-102 (CDR3). In addition mouse residues were used
CC in the frameworks at positions 48, 67, 69, 71, 73, 76, 89, 91, 94 and 108.
CC Comparison of the hTNF1 mouse and EU human heavy chain residues
CC reveals that these are identical at positions 23, 24, 29, and 78.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 121 AA;
SQ
Query Match 79.5%; Score 356; DB 13; Length 121;
Best Local Similarity 61.2%; Pred. No. 4.5e-26;
Matches 74; Conservative 10; Mismatches 3; Indels 34; Gaps 3;
QY 1 QIQLVQSGGELVKGASVYVSCKASGYSTFT-----WYQSPFGKLEWIG----- 43
1 QVQLVQSGAEVYKPGSSVYVSCKASGYSTFTDYNVDVYKQAPQGLQWIGINPNNGGTY 60
Db 44 -----GRATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 86
61 NQKFKGKGLTVDKSTSTAYMELSSLRSEDTAVYCARSAFYNNYEDYVWQGTITVTVSS 120
QY 87 S 87
Db 121 S 121

RESULT 9
AA71548
ID AA71548 standard; Protein; 136 AA.
XX
XX AA71548;
XX

DT 12-OCT-2000 (first entry)
 XX Humanised antibody HuZAF, heavy chain variable region (HuZAF-VH).
 XX
 XX Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; VL;
 KW light chain variable region; VH; heavy chain variable region; HuZAF-VH;
 KW gamma-interferon; IFN; complementarity determining region; CDR; FR;
 KW framework region; immunosuppressive; antineoplastic; antileukemic;
 KW gastrointestinal; antidiabetic; antithrombotic; antineoplastic; inhibitor;
 KW autoimmune disease; graft versus host disease; organ transplant; IgG1;
 KW multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;
 KW systemic lupus erythematosus; SLE; Crohn's disease.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..19
 FT /note= "N-terminal peptide"
 FT
 FT Protein 20..136
 FT /note= "Mature humanised antibody HuZAF heavy chain
 FT variable region (HuZAF-VH)"
 FT
 FT Misc-difference 30
 FT /note= "Corresponds to position 11 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 46
 FT /note= "Corresponds to position 27 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 47
 FT /note= "Corresponds to position 28 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 49
 FT /note= "Corresponds to position 30 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Region 50..54
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT
 FT Misc-difference 57
 FT /note= "Corresponds to position 38 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 67
 FT /note= "Corresponds to position 48 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Region 69..85
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT
 FT Misc-difference 86
 FT /note= "Corresponds to position 67 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 87
 FT /note= "Corresponds to position 68 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 89
 FT /note= "Corresponds to position 70 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 91
 FT /note= "Corresponds to position 72 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 93
 FT /note= "Corresponds to position 74 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 112

FT /note= "Corresponds to position 93 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 114
 FT /note= "Corresponds to position 95 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 117
 FT /note= "Corresponds to position 98 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Region 118..125
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT
 FT Misc-difference 126
 FT /note= "Corresponds to position 107 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 127
 FT /note= "Corresponds to position 108 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 128
 FT /note= "Corresponds to position 109 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT Misc-difference 130
 FT /note= "Corresponds to position 111 of mature HuZAF-VH,
 FT substituted with residue at equivalent position of mouse
 FT mature AF2 antibody heavy chain (VH)"
 FT
 FT WO2000032634-A1.
 PN 08-JUN-2000.
 XX 29-NOV-1999; 99WO-US28195.
 XX 01-DEC-1998; 98US-0110523.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;
 FI WPI; 2000-412292/35.
 DR N-PSDB; AAD01348.
 DR
 PT Humanized murine AF2 immunoglobulins, useful for inhibiting
 PT gamma-interferon for the treatment of autoimmune diseases, e.g.
 PT multiple sclerosis and diabetes -
 XX
 XX Claim 10; Fig 2B; 32pp; English.
 XX
 CC The present amino acid sequence is the humanised version of the mouse AF2
 CC immunoglobulin, HuZAF heavy chain variable region (HuZAF-VH), of IgG1
 CC isotype. The humanised HuZAF antibody comprises mouse AF2 antibody
 CC complementarity determining regions (CDRs), functionally joined to the
 CC human acceptor antibody EU framework regions (FR). Mature HuZAF-VH FR at
 CC positions 11, 27, 28, 30, 38, 48, 67, 68, 70, 72, 74, 93, 95, 98, 107,
 CC 108, 109 and 111 are occupied by residues present in the equivalent
 CC positions of the mouse mature AF2 heavy chain variable region (VH).
 CC HuZAF antibody specifically binds to and neutralises gamma-interferon
 CC (IFN). They can also block the binding of mouse AF2 immunoglobulin to
 CC gamma-IFN. HuZAF does not contain sequences that are immunogenically
 CC active in humans and remains unaffected by immune responses, that may
 CC reduce its activity or circulating half-life. HuZAF may be administered
 CC to treat autoimmune diseases such as graft versus host disease following
 CC organ transplant, Type I diabetes, multiple sclerosis, rheumatoid
 CC arthritis, psoriasis, systemic lupus erythematosus (SLE), Hashimoto's
 CC thyroiditis, primary biliary cirrhosis and inflammatory bowel disease
 CC like, Crohn's disease.
 XX
 SQ Sequence 136 AA;

Query Match 79.5%; Score 356; DB 21; Length 136;
 Best Local Similarity 64.1%; Pred. No. 5e-26;
 Matches 75; Conservative 8; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYST-----WVRQSPGKGLWGT----- 44
 DB 20 QVQLVQSGAELKPGSSVKVSKASGYFTSNWNVKQAPGGGLEWIGRIDPSGEVHY 79
 QY 45 -----KATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WQGQITVTVSS 87
 DB 80 NQDFKDKATLTVDKSTNTAYMELSSLRSEDTAVYFCARGLFWFADWQGQITVTVSS 136

RESULT 10
 AAW90935
 ID AAW90935 standard; Protein; 470 AA.
 XX AC AAW90935;
 XX DT 08-AUG-2000 (first entry)
 XX DE Humanised anti-Fas designed heavy chain Heu 3 protein.
 XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatocytic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; Glomerulonephritis; hepatitis; transplant rejection.
 XX OS Synthetic.
 XX PN EP990663-A2.
 XX PD 05-APR-2000.
 XX PF 29-SEP-1999; 99EP-0307711.
 XX PR 30-SEP-1998; 98JP-0276881.
 XX PR 30-SEP-1998; 98JP-0276882.
 XX PA (SANY) SANKYO CO LTD.
 XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 XX N-PSDB; AAA11646.
 XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX PS Claim 2; Page 180-182; 263pp; English.
 XX CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, chymotremetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 79.0%; Score 354; DB 21; Length 470;
 Best Local Similarity 62.0%; Pred. No. 2.6e-25;
 Matches 75; Conservative 8; Mismatches 4; Indels 34; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRVSKASGYST-----WVRQSPGKGLWGT----- 43
 DB 20 QVQLVQSGAELKPGSSVKVSKASGYFTSYWQVVRQAPGGGLEWIGRIDPSDYTN 79
 QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WQGQITVTVSS 86
 DB 80 NQDFKDKATLTVDKSTNTAYMELSSLRSEDTAVYFCARGLFWFADWQGQITVTVSS 139
 QY 87 S 87
 DB 140 S 140

RESULT 11

ABE74904
 ID ABE74904 standard; Protein; 470 AA.

XX AC ABE74904;
 XX DT 26-APR-2002 (first entry)
 XX DE Mouse humanised anti-Fas antibody related protein SEQ ID NO 9.
 XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
 KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
 KW autoimmune disease; allergy; atopic.
 XX OS Mus musculus.
 XX PN JP2001342148-A.
 XX PD 11-DEC-2001.
 XX PF 28-MAR-2001; 2001JP-0093106.
 XX PR 29-MAR-2000; 2000JP-0090918.
 XX PA (SANY) SANKYO CO LTD.
 XX WPI; 2002-1451113/19.
 XX N-PSDB; ABL45926.
 XX PT Drug containing humanised anti-Fas antibody, used for preventing and
 PT treating autoimmune diseases, allergy, and atopy -
 XX PS Example 4 (Preparatory); Page 79-80; 194pp; Japanese.

CC The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in Fas/Fas ligand system containing as the active
 CC component an antibody having as the light chain subunit a polypeptide
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 CC fully defined in the specification and having an activity of combining

CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
CC lymphocytic leukaemia.

XX Sequence 116 AA;

XX Query Match 78.9%; Score 353.5; DB 18; Length 116;

XX Best Local Similarity 62.9%; Pred. No. 7.3e-26;
XX Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 44

DB 1 QVQLVSGAEVKKPGSSVKVSKASGYTTSYHLHWVRQAPGQGLEWIGYINPRNDYTEY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAYFCAR-----WGQGTITVTVSS 87

DB 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTITVTVSS 116

RESULT 14

AAR29017
ID AAR29017 standard; Protein; 135 AA.

XX AC AAR29017;

XX DT 25-MAR-2003 (updated)

XX DT 30-MAR-1993 (first entry)

XX DE pUC-RVh-1220d.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
XX complementarity determining region; monoclonal; hybridoma; PCR;
XX plasmid; polymerase chain reaction; amplify.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..19 /note= "Leader peptide"

FT Region 20..49 /label= FR1

FT Region 50..54 /label= CDR1

FT Region 55..68 /label= FR2

FT Region 69..85 /label= CDR2

FT Region 86..117 /label= FR3

FT Region 118..124 /label= CDR3

FT Region 125..135 /label= FR4

XX WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP00544.

XX 25-APR-1991; 91JP-0095476.

XX 13-FEB-1992; 92JP-0032064.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Bendig MM, Jones ST, Saldanha JW, Sato K, Teuchiya M;

XX WPI; 1992-398882/48.

XX N-PSDB; AAQ31391.

XX Reconstituted human antibody to human interleukin-6 receptor -

XX has low antigenicity and contains mouse V-region complementarity

XX determining regions

PS Disclosure; Page 159-60; 207pp; Japanese.

XX The sequences given in AAR29016-17 are portions of monoclonal antibodies
XX which were encoded by plasmids contained within the mouse hybridoma,
XX AUK12-20. The DNA encoding the complementarity determining regions
XX (CDR's) was isolated by polymerase chain reaction. These antibodies
XX recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
XX were transformed with plasmids containing fragments of the antibody
XX gene which caused the production of the antibody from the hybridoma
XX cell line.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 135 AA;

XX Query Match 78.9%; Score 353.5; DB 13; Length 135;

XX Best Local Similarity 63.8%; Pred. No. 8.5e-26;
XX Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIOLVSGGELVKPGASVRVSKASGYST-----WVROSPGKGLWIG----- 43

DB 20 QVQLVSGAEVKKPGASVRVSKASGYSTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAYFCAR-----WGQGTITVTVSS 87

DB 80 NQKPKGKVTMTVDSTNTAYMELSSLRSEDTAVVYCARCGNRFAYWGQGTITVTVSS 135

RESULT 15

AAW65773

ID AAW65773 standard; Protein; 139 AA.

XX AC AAW65773;

XX DT 16-NOV-1998 (first entry)

XX DE Anti-human HM1.24 antibody heavy chain variable region r.

XX Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;
XX pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..19 /note= "Signal peptide"

FT Peptide 20..139 /note= "Mature peptide"

XX WO9835698-A1.

XX 20-AUG-1998.

XX 12-FEB-1998; 98WO-JP00568.

XX 12-FEB-1997; 97JP-0041410.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Koishihara Y, Yoshimura Y;

XX WPI; 1998-456869/39.

XX N-PSDB; AAV07581.

XX Treatment of lymphocytic tumours using cytotoxic antibody - binding

XX to specific antigen such as HM1.24 and effective against T-cell

XX tumours and B-cell tumours other than myeloma

XX Disclosure; Page 47-48; 82pp; Japanese.

XX The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be

XX used in the treatment of lymphocytic tumours, including T-cell tumours

XX and B-cell tumours other than myeloma. The antibody is preferably

XX monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or

CC humanised, and preferably contains a human antibody constant region C
CC gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an
CC anti-human Hm1.24 antibody or an antibody which binds to an epitope
CC recognising anti-human Hm1.24 antibody. The cytotoxic antibody is useful
CC in the treatment of lymphocytic tumours such as acute or chronic B
CC lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or
CC chronic T lymphocytic leukaemia.
XX
SQ Sequence 139 AA;

Query Match 78.9%; Score 353.5; DB 19; Length 139;
Best Local Similarity 60.8%; Pred. No. 8.8e-26;
Matches 73; Conservative 10; Mismatches 4; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYST-----WVRQSPCKGLEW----- 43
DB 20 QVQLVQSGAEVKKPGASVKVCKASGYTFTPYWMQWVRQAPGQGLEWNGSIFPGDGDTRY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDTAIFYFCAR-----WQGGTIVTVSS 87
DB 80 SQKFKGRVTMTADKSTSTAYMELSLRSEDTAIFYFCARGLRGGYFDYWGQGTIVTVSS 139

Search completed: January 13, 2004, 12:38:24
Job time : 21.2873 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 13.9048 Seconds
(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 QIQLVQSGGELVKPGASVRV.....DTAVVFCARWGQGTIVTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	87	11	US-09-990-586-90
2	448	100.0	87	12	US-10-230-880-90
3	440	98.2	87	12	US-09-990-586-95
4	440	98.2	87	12	US-10-230-880-95
5	439	98.0	87	11	US-09-990-586-89
6	439	98.0	87	11	US-09-990-586-91
7	439	98.0	87	11	US-09-990-586-92
8	439	98.0	87	12	US-10-230-880-89
9	439	98.0	87	12	US-10-230-880-91
10	439	98.0	87	12	US-10-230-880-92
11	437	97.5	87	11	US-09-990-586-96
12	437	97.5	87	12	US-10-230-880-96
13	434	96.9	87	11	US-09-990-586-94
14	434	96.9	87	12	US-10-230-880-94
15	431	96.2	87	11	US-09-990-586-93

Sequence 93, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 166, App
Sequence 172, App
Sequence 85, Appl
Sequence 158, App
Sequence 167, App
Sequence 200, App
Sequence 159, App
Sequence 171, App
Sequence 84, Appl
Sequence 157, App
Sequence 160, App
Sequence 7, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 24, Appl
Sequence 78, Appl
Sequence 63, Appl
Sequence 199, App

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US-10-412-703A-7
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US-10-230-880-83
US-10-230-880-165
US-10-223-880-5
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US-09-556-206A-78
US-09-556-206A-63
US-09-509-098-199

431 96.2 87 12
426 95.1 87 11
426 95.1 87 12
415 92.6 87 11
415 92.6 87 12
407 90.8 87 11
407 90.8 87 12
405 90.4 87 12
405 90.4 87 12
394 87.9 87 11
394 87.9 87 12
390 87.1 87 12
387 86.4 87 12
382 85.3 87 11
380 84.8 87 12
379 84.6 87 11
379 84.6 87 12
377 84.2 87 12
377 84.2 87 12
373 83.3 87 11
373 83.3 87 12
367 81.9 87 12
365 81.5 117 12
360.5 80.5 135 10
360.5 80.5 461 10
360 80.4 117 10
360 80.4 136 10
356 79.5 87 11

ALIGNMENTS

RESULT 1

US-09-990-586-90

; Sequence 90, Application US/0990586

; Publication No. US20030109680A1

; GENERAL INFORMATION:

; APPLICANT: JIAO, JIN-AN

; APPLICANT: WONG, HING C

; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

; TITLE OF INVENTION: OF USE THEREOF

; FILE REFERENCE: 71758/46943-CIP2

; CURRENT APPLICATION NUMBER: US/09/990,586

; CURRENT FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 09/293,854

; PRIOR FILING DATE: 1999-04-16

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 90

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-990-586-90

Query Match 100.0%; Score 448; DB 11; Length 87;

Best Local Similarity 100.0%; Pred. No. 2.9e-37;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVCKASGYFTVWRQSPGKLEWIGKATLTVDKSTSTAYME 60

DB 1 QIQLVQSGGELVKPGASVRVCKASGYFTVWRQSPGKLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVVFCARWGQGTIVTVSS 87

DB 61 LSSLRSEDTAVVFCARWGQGTIVTVSS 87

RESULT 2

US-10-230-880-90

; Sequence 90, Application US/10230880

```

/ Publication No. US20030190705A1
/
/ GENERAL INFORMATION:
/ APPLICANT: WONG, HING C.
/ APPLICANT: STINSON, JEFFREY L.
/ APPLICANT: MOSQUERA, LUIS A.
/ TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
/ FILE REFERENCE: 71758/58066
/ CURRENT APPLICATION NUMBER: US/10/230,880
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: 09/990,586
/ PRIOR APPLICATION NUMBER: 60/343,306
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 09/293,854
/ PRIOR FILING DATE: 1999-04-16
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 90
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-230-880-90

```

```

Query Match      100.0%; Score 448, DB 12; Length 87;
Best Local Similarity 100.0%; Pred. NO. 2.9e-37;
Matches 87; Conservative 0; Mismatches 0; Gaps 0;

QY 1 QIQLVOSGGELVFKPGASVRYSCASGYSPFWVRQSPGKLEWIGKATITVDKNSTAYWE 60
Db 1 QIQLVOSGGELVFKPGASVRYSCASGYSPFWVRQSPGKLEWIGKATITVDKNSTAYWE 60

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Qy 61 LSSLRSEDTAVYFCARWGQGTIVSS 87
 |||||
 Db 61 LSSLRSEDTAVYFCARWGQGTIVSS 87

```

RESULT 3
US-09-990-586-95
; Sequence 95, Application US/09990586
; Publication NO. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-95

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Query Match	98.2%	Score	440	DB	11	Length	87
Best Local Similarity	98.5%	Pred.No.	1.8e-36				
Matches	86	Conservative	0	Mismatches	1	Indels	0
Gaps	0						
QY	1	QIQVQSGGELVPGASVVRVSKASGYGVSFTVVRQSPGKGLEWIGKATITVVKSTSTAYME	60				
Db	1	QIQVQSGFELVPGASVVRVSKASGYGVSFTVVRQSPGKGLEWIGKATITVVKSTSTAYME	60				
QY	61	IGSLRSEDATVYFCARWGQGTITVVS	87				
Db	61	IGSLRSEDATVYFCARWGQGTITVVS	87				

RESULT 4
US-10-230-880-95

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/ Sequence 95, Application US/10230880
/ Publication No. US20030190705A1
/ GENERAL INFORMATION:
/ APPLICANT: WONG, HING C.
/ APPLICANT: STINSON, JEFFREY L.
/ APPLICANT: MOSQUERA, LUIS A.
/ TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
/ FILE REFERENCE: 71758/58066
/ CURRENT APPLICATION NUMBER: US/10/230,880
/ CURRENT FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: 09/990,586
/ PRIOR FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: 60/343,306
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: 09/293,854
/ PRIOR FILING DATE: 1999-04-16
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn ver. 2.1
/ SEQ ID NO 95
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-230-880-95

```

Query Match	98.2%	Score 440;	DB 12;	Length 87;
Best Local Similarity	98.9%	Pred. No. 1.8e-36;		
Matches	86;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
Qy 1	QIQLVSGGELVKPGASVRVSCAKSYSTFWQSPGKLEWIGKATLV	VDKSTSYAYME	60	
cb 1	QIQLVSGGELVKPGASVRVSCAKSYSTFWQSPGKLEWIGKATLV	VDKSTSYAYME	60	

Qy 61 LSSLRSEDTAVYFCARWGQGITTVSS 87
|||
pb 61 LSSLRSEDTAVYFCARWGQGITTVSS 87

RESULT 5
 US-09-990-586-89
 ; Sequence 89, Application US/09990586
 ; Publication No. US20030109680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JIAO, JIN-AN
 ; APPLICANT: WONG, HING C.
 ; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
 ; TITLE OF INVENTION: OF USE THEREOF
 ; FILE REFERENCE: 71758/45943-CIP2
 ; CURRENT APPLICATION NUMBER: US/09/990,586
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 09/293,854
 ; PRIOR FILING DATE: 1999-04-16
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 89
 ; LENGTH: 87
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-990-586-89

```
Query Match      98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred.No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QIOLVGGSELVPGASVRVSCKASGYSFVTWVQSPOKGLEWGKATLTVDKSTSYAME 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 QMQLQGSGBELVPGASVRVSCKASGYSFVTWVQSPOKGLEWGKATLTVDKSTSYAME 60

Qy 61 LSSLRSDDTAVYFCARWGQGTITTVSS 87
Db 61 LSLRSDDTAVYFCARWGQGTITTVSS 87
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RESULT 6

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US-09-990-586-91
; Sequence 91, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-91

Query Match      98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 7
US-09-990-586-92
; Sequence 92, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-92

Query Match      98.0%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 8
US-10-230-880-89
; Sequence 89, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-91

Query Match      98.0%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 9
US-10-230-880-91
; Sequence 91, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-91

Query Match      98.0%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGELVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGEVKPGASVRVSCKASGYSTFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
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RESULT 10

US-10-230-880-92
; Sequence 92, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 92
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-92

Query Match 98.0%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

RESULT 11

US-09-990-586-96
; Sequence 96, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 96
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-96

Query Match 97.5%; Score 437; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 3.6e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

RESULT 12

US-10-230-880-96
; Sequence 96, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 96
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-96

Query Match 97.5%; Score 437; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 3.6e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVSGGEVVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87
DB 61 LSSLRSEDATVYFCARWGQTTVTSS 87

RESULT 13

US-09-990-586-94
; Sequence 94, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 94
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-94

Query Match 96.9%; Score 434; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 7.2e-36;
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGELVKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVSGPELKKPGASVRVSCASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSEDATVYFCARWGQTTVTSS 87

Db 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

Search completed: January 13, 2004, 13:13:43
Job time : 13.9048 secs

Db 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

RESULT 14

US-10-230-880-94
; Sequence 94, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-94

Query Match 96.9%; Score 434; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 7.2e-36;
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QIQLVQSGGELVPGASVRVSCASGYSTFWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
Db 1 QIQLVQSGPBLKPKGASVRVSCASGYSTFWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

Qy 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87
Db 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

RESULT 15

US-09-990-586-93
; Sequence 93, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-93

Query Match 96.2%; Score 431; DB 11; Length 87;
Best Local Similarity 96.6%; Pred. No. 1.4e-35;
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QIQLVQSGGELVPGASVRVSCASGYSTFWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
Db 1 QIQLVQSGPEVKPKGASVRVSCASGYSTFWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60

Qy 61 LSSLRSEDVAVFCARWGQGTTVTVSS 87

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 7.52227 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-90

Perfect score: 448

Sequence: 1 Q1QLVSGGLVPGASVRV.....DTAVYFCARWGQTTVTSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	376	83.9	87	1	US-08-497-312-16
2	360	80.4	117	4	US-08-525-539A-78
3	360	80.4	136	4	US-08-525-539A-63
4	356	79.5	136	4	US-08-450-520A-8
5	354.5	79.1	86	1	US-08-497-312-27
6	353.5	78.9	116	1	US-08-690-102A-8
7	353.5	78.9	116	3	US-09-127-902-8
8	353.5	78.9	116	3	US-09-135-107-8
9	353.5	78.9	116	5	PCT-US95-09641-8
10	353.5	78.9	135	1	US-08-137-117D-102
11	353.5	78.9	135	2	US-08-436-717-102
12	353.5	78.9	139	4	US-09-355-925-7
13	353.5	78.9	139	4	US-09-355-925-8
14	352.5	78.7	116	2	US-08-561-521-41
15	352.5	78.7	116	5	PCT-US95-01219-41
16	350.5	78.2	116	1	US-08-488-113B-168
17	350.5	78.2	116	1	US-08-477-484B-168
18	350.5	78.2	116	1	US-08-107-669D-54
19	350.5	78.2	116	1	US-08-472-788A-54
20	350.5	78.2	116	2	US-08-477-531B-54
21	350.5	78.2	116	2	US-08-646-360-168
22	350.5	78.2	116	2	US-08-082-842A-54
23	350.5	78.2	116	3	US-08-839-765-168
24	350.5	78.2	116	3	US-09-136-389-168
25	350.5	78.2	116	4	US-09-610-838-168
26	350	78.1	119	1	US-08-458-516-10
27	350	78.1	222	1	US-08-458-516-22

28	350	78.1	235	1	US-08-458-516-23
29	350	78.1	449	1	US-08-458-516-13
30	349.5	78.0	116	1	US-07-634-278-5
31	349.5	78.0	116	1	US-07-634-278-57
32	349.5	78.0	116	1	US-07-634-278-73
33	349.5	78.0	116	1	US-08-477-728-5
34	349.5	78.0	116	1	US-08-477-728-57
35	349.5	78.0	116	1	US-08-477-728-73
36	349.5	78.0	116	1	US-08-474-040-5
37	349.5	78.0	116	1	US-08-474-040-57
38	349.5	78.0	116	1	US-08-474-040-73
39	349.5	78.0	116	1	US-08-487-200-5
40	349.5	78.0	116	1	US-08-487-200-57
41	349.5	78.0	116	1	US-08-487-200-73
42	349.5	78.0	116	1	US-08-488-113B-169
43	349.5	78.0	116	1	US-08-477-484B-169
44	349.5	78.0	116	1	US-08-107-669D-55
45	349.5	78.0	116	1	US-08-472-788A-86

ALIGNMENTS

RESULT 1

US-08-497-312-16
; Sequence 16, Application US/08497312
; Patent No. 5712120

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Method for obtaining modified

TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

STREET: 215 Y 15, ATABEY PLAYA

CITY: HAVANA

STATE:

COUNTRY: CUBA

ZIP: 11600

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,312

FILING DATE: 30-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CU 80/94

FILING DATE: 30-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: BOND, LAURENCE B.

REGISTRATION NUMBER: 30,549

REFERENCE/DOCKET NUMBER: 2629US

TELEPHONE: 801/532-1922

TELEFAX: 801/531-9168

TELEX: 388961 LPMO4UT

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 87 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-08-497-312-16

Query Match 83.9%; Score 376; DB 1; Length 87;

Best Local Similarity 79.3%; Pred. No. 1e-31;

Matches 69; Conservative 10; Mismatches 8; Indels 0; Gaps 0;


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QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLVDSKSTAYME 60
Db 1 QVQLVQSGAEVKPGASVRSCKASGYTFNWRQAPGQGLEWVGRVTRDTSTSTVME 60
QY 61 LSSLRSSEDTAVYFCARWGQGTIVTVSS 87
Db 61 LSSLRSSEDTAVYFCARWGQGTIVTVSS 87

RESULT 2
US-08-525-539A-78
; Sequence 78, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-78

Query Match 80.4%; Score 360; DB 4; Length 117;
Best Local Similarity 65.8%; Pred. No. 6.1e-30;
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFWRSQPGKLEWIG-----WVRSQPGKLEWIG----- 44
Db 1 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTMHWYKQSPGMNLEWIGLINFYNGGTVY 60
QY 45 -----KATLVDSKSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFDKATLVDSKSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTIVTVSS 117

RESULT 3
US-08-525-539A-63
; Sequence 63, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.

```

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; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-63

Query Match 80.4%; Score 360; DB 4; Length 136;
Best Local Similarity 65.8%; Pred. No. 7.2e-30;
Matches 77; Conservative 5; Mismatches 5; Indels 30; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSTFWRSQPGKLEWIG-----WVRSQPGKLEWIG----- 44
Db 20 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTMHWYKQSPGMNLEWIGLINFYNGGTVY 79
QY 45 -----KATLVDSKSTAYMELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87
Db 80 NQKFDKATLVDSKSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTIVTVSS 136

RESULT 4
US-09-450-520A-8
; Sequence 8, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/450,520A
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/110,523
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: Description of Artificial Sequence: human-mouse
 OTHER INFORMATION: transgenic construct HuZAF VH
 US-09-450-520A-8

Query Match 79.5%; Score 356; DB 4; Length 136;
 Best Local Similarity 64.1%; Pred. No. 1.8e-29;
 Matches 75; Conservative 8; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFT-----WVROSPGKGLWIG----- 44
 Db 20 QVQLVSGAELKPGASVKVSKASGYFTSSWINVWKPAPGGLEWIGRIDPSDEVHY 79
 QY 45 -----KATLVDKSTSTAYMELSLRSEDYAVFCAR-----WGQTTVTWSS 87
 Db 80 NQDFKDKATLVDKSTNTAYMELSLRSEDYAVYCARGLPWFADWGQGLTVTVSS 136

RESULT 5
 US-08-497-312-27
 ; Sequence 27, Application US/08497312
 ; Patent No. 5712120
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Method for obtaining modified
 ; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
 ; TITLE OF INVENTION: antibody variable domains, compositions containing them.
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
 ; STREET: 215 Y 15, ATABEY PLAYA
 ; CITY: HAVANA
 ; STATE:
 ; COUNTRY: CUBA
 ; ZIP: 11600
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/497,312
 ; FILING DATE: 30-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: CU 80/94
 ; FILING DATE: 30-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BOND, LAURENCE B.
 ; REGISTRATION NUMBER: 30,549
 ; REFERENCE/DOCKET NUMBER: 2629US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 801/531-9168
 ; TELEFAX: 801/531-9168
 ; TELEX: 388961 1PMO4UT
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 86 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-08-497-312-27

Query Match 79.1%; Score 354.5; DB 1; Length 86;
 Best Local Similarity 77.0%; Pred. No. 1.6e-29;
 Matches 67; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFTWVROSPGKGLWIGKATLVDKSTSTAYME 60
 Db 1 QVQLVSGAEVKKPGASLVSKASGY-FTWVROAPQRLWNGRVTITRDTASTAYME 59
 QY 61 LSSLRSEDYAVYFCARWGQTTVTWSS 87

Db 60 LSSLRSEDYAVYFCARWGQTTVTWSS 86

RESULT 6

US-08-690-102A-8
 ; Sequence 8, Application US/08690102A
 ; Patent No. 5789554
 ; GENERAL INFORMATION:
 ; APPLICANT: LEUNG, Shui-on
 ; APPLICANT: HANSEN, Hans
 ; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/690,102A
 ; FILING DATE: 01-JUL-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,576
 ; FILING DATE: 12-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAXE, Bernhard D.
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 18733/453/IMIN
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; TELEX: 904136
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-690-102A-8

Query Match 78.9%; Score 353.5; DB 1; Length 116;
 Best Local Similarity 62.9%; Pred. No. 2.8e-29;
 Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVSGGELVKPGASVRVSKASGYSFT-----WVROSPGKGLWIG----- 44
 Db 1 QVQLVSGAEVKKPGSSVKVSKASGYFTTSYWLHWVRQAPGQGLEWIGYINPRNDYTEY 60
 QY 45 -----KATLVDKSTSTAYMELSLRSEDYAVFCAR-----WGQTTVTWSS 87
 Db 61 NQNFKDKATITADESTNTAYMELSLRSEDYAVFCARDITTFYWGQGTITVTWSS 116

RESULT 7

US-09-127-902-8
 ; Sequence 8, Application US/09127902
 ; Patent No. 6187287
 ; GENERAL INFORMATION:
 ; APPLICANT: LEUNG, Shui-on
 ; APPLICANT: HANSEN, Hans
 ; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/127,902
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/690,102
 FILING DATE: 01-JUL-1996
 APPLICATION NUMBER: US 08/289,576
 FILING DATE: 12-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: SAXE, Bernhard D.
 REGISTRATION NUMBER: 28,665
 REFERENCE/DOCKET NUMBER: 18733/463/IMIN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 9041136
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-127-902-8

Query Match 78.9%; Score 353.5; DB 3; Length 116;
 Best Local Similarity 62.9%; Pred. No. 2.8e-29;
 Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;
 QY 1 QIQLVQSGGELVKPGASRVKSCASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 44
 DB 1 QVQLVQSGAEVKPGSSVKVSKASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAVYFCARRDITTFYWGQGTITVTVSS 116
 RESULT 8
 US-09-155-107-8
 ; Sequence 8, Application US/09155107
 ; Patent No. 6254868
 ; GENERAL INFORMATION:
 ; APPLICANT: LEUNG, Shui-on
 ; APPLICANT: HANSEN, Hans
 ; APPLICANT: QU, Zhengxing
 ; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
 ; FILE REFERENCE: 018733/0879
 ; CURRENT APPLICATION NUMBER: US/09/155,107
 ; CURRENT FILING DATE: 1998-11-17
 ; EARLIER APPLICATION NUMBER: WO PCT/US97/04196
 ; EARLIER FILING DATE: 1997-03-19
 ; EARLIER APPLICATION NUMBER: US 60/013,709
 ; EARLIER FILING DATE: 1996-03-20
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 116
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-155-107-8

Query Match 78.9%; Score 353.5; DB 3; Length 116;
 Best Local Similarity 62.9%; Pred. No. 2.8e-29;
 Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASRVKSCASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 44
 DB 1 QVQLVQSGAEVKPGSSVKVSKASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAVYFCARRDITTFYWGQGTITVTVSS 116

RESULT 9
 PCT-US95-09641-8
 ; Sequence 8, Application PC/TUS9509641
 ; GENERAL INFORMATION:
 ; APPLICANT: IMMUNOCONJUGATES AND HUMANIZED
 ; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
 ; NUMBER OF SEQUENCES: 21
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/09641
 ; FILING DATE: 11-AUG-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/289,576
 ; FILING DATE: 12-AUG-1994
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 116 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-09641-8

Query Match 78.9%; Score 353.5; DB 5; Length 116;
 Best Local Similarity 62.9%; Pred. No. 2.8e-29;
 Matches 73; Conservative 10; Mismatches 4; Indels 29; Gaps 3;
 QY 1 QIQLVQSGGELVKPGASRVKSCASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 44
 DB 1 QVQLVQSGAEVKPGSSVKVSKASGYFTTYSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
 QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
 DB 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAVYFCARRDITTFYWGQGTITVTVSS 116

RESULT 10
 US-08-137-117D-102
 ; Sequence 102, Application US/08137117D
 ; Patent No. 5795965
 ; GENERAL INFORMATION:
 ; APPLICANT: TSUCHIYA, Masayuki
 ; APPLICANT: SATO, Koh
 ; APPLICANT: BENDIG, Mary
 ; APPLICANT: JONES, Steven
 ; APPLICANT: SALDANHA, Jose
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
 ; INTERLEUKIN-6 RECEPTOR
 ; NUMBER OF SEQUENCES: 158
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,259
REFERENCE/DOCKET NUMBER: 53466/126/RAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 78.9%; Score 353.5; DB 1; Length 135;
Best Local Similarity 63.8%; Pred. No. 3.3e-29;
Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI-----43
Db 20 QVQLVQSGAEVKPKGASVKVSKASGYSFTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79
QY 44 -----GKATLVDSKSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87
Db 80 NQKFKGKVTMTVDSTNTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 135

RESULT 11
US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALLANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/RAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-102

Query Match 78.9%; Score 353.5; DB 2; Length 135;
Best Local Similarity 63.8%; Pred. No. 3.3e-29;
Matches 74; Conservative 8; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI-----43
Db 20 QVQLVQSGAEVKPKGASVKVSKASGYSFTSYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79
QY 44 -----GKATLVDSKSTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 87
Db 80 NQKFKGKVTMTVDSTNTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 135

RESULT 12
US-09-355-925-7
Sequence 7, Application US/09355925
Patent No. 6503510
GENERAL INFORMATION:
APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUSHI
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 7
LENGTH: 139
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence of H chain V region version r of
OTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7

Query Match 78.9%; Score 353.5; DB 4; Length 139;
Best Local Similarity 60.8%; Pred. No. 3.4e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 33; Gaps 3;

QY 1 QIQLVQSGGELVKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI-----43
Db 80 NQKFKGKVTMTVDSTNTAYMELSLRSEDATVYFCAR-----WGQGTIVTVSS 135

DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFPTVMQWVRQAPQGGLWNGSIFPGGDTRY 79
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
DB 80 SQKFQKRVITADKSTAYMELSLRSEDATVYFCARGLRGGYFDYWGQGTITVTVSS 139

RESULT 13
US-09-355-925-8
; Sequence 8, Application US/093555925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053465/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 8
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence H chain V region version 8 of
; OTHER INFORMATION: anti-HM1.24 antibody
US-09-355-925-8

Query Match 78.9%; Score 353.5; DB 4; Length 139;
Best Local Similarity 60.8%; Pred. No. 3.4e-29;
Matches 73; Conservative 10; Mismatches 4; Indels 33; Gaps 3;

QY 1 QIQLVQSGELVKPGASVRSCKASGYST-----WVRSPPGKLEWI-----43
DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFPTVMQWVRQAPQGGLWNGSIFPGGDTRY 79
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
DB 80 SQKFQKRVITADKSTAYMELSLRSEDATVYFCARGLRGGYFDYWGQGTITVTVSS 139

RESULT 14
US-08-561-521-41
; Sequence 41, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; FILING DATE: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:

; FILING DATE: 424
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-41

Query Match 78.7%; Score 352.5; DB 2; Length 116;
Best Local Similarity 62.9%; Pred. No. 3.5e-29;
Matches 73; Conservative 9; Mismatches 5; Indels 29; Gaps 3;

QY 1 QIQLVQSGELVKPGASVRSCKASGYST-----WVRSPPGKLEWI-----43
DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYSTFYIHWRQAPQGGLWNGSIFPGGDTRY 60
QY 44 -----GKATLTVDKSTAYMELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
DB 61 NQKFKGVITVDKSTAYMELSLRSEDATVYFCARGLRGGYFDYWGQGTITVTVSS 116

RESULT 15
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-41

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Query Match      78.7%  Score 352.5;  DB 5;  Length 116;
Best Local Similarity  52.9%  Pred. No. 3.5e-29;
Matches 73;  Conservative 9;  Mismatches 5;  Indels 29;  Gaps 3;

Qy  1 QIQLVQSGGELVPGASRVVSCXASGYST-----WVRSFGKGLWFI----- 43
Db  1 QVQLVQSGAEVKKFGASVKVSCXASGYSTSYIHWVRQAPGQGLEWVGYIDPFNGGTSY 60
Qy  44 -----GKATLTVDKSTSTAYMELSSLSRSEDYAVVFCAR-----WGQGTITVTVSS 87
Db  61 NQKFKGVTVTVDTSTNTAYMELSSLSRSEDYAVYCARGGNRFAYWQGTITVTVSS 116

```

Search completed: January 13, 2004, 12:46:32
Job time : 7.52227 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 6.30655 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQLVQSGGVKPGASVRV.....DTAVFCARWGQTTVTYSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	347	77.3	119	2 PH0961	Ig heavy chain V r
2	345.5	76.3	122	2 PH0958	Ig heavy chain V r
3	344.5	76.7	118	2 S36265	Ig heavy chain V r
4	342.5	76.3	116	2 PH0959	Ig heavy chain V r
5	342.5	76.3	136	2 PH0960	Ig heavy chain V r
6	341	75.9	142	2 A32483	Ig heavy chain V r
7	340.5	75.8	120	2 PH0962	Ig heavy chain V r
8	340.5	75.8	128	2 PH0952	Ig heavy chain V r
9	340.5	75.8	132	2 PH0954	Ig heavy chain V r
10	339	75.5	127	2 PH0955	Ig heavy chain V r
11	337	75.1	133	2 C33548	Ig heavy chain V-1
12	337	75.1	627	2 S14683	Ig mu chain precuor
13	336.5	74.9	119	2 A24672	Ig heavy chain pre
14	336.5	74.9	126	2 B33548	Ig heavy chain V-1
15	336.5	74.9	135	2 S49330	anti-Sm antibody V
16	336	74.8	129	2 A33548	Ig heavy chain V-1
17	335	74.6	121	2 S20783	Ig heavy chain V r
18	335	74.6	129	2 S36260	Ig heavy chain V r
19	334.5	74.5	469	2 S37483	Ig gamma-2a chain
20	334	74.4	125	2 PH0957	Ig heavy chain V r
21	333.5	74.3	124	2 S19665	Ig heavy chain V r
22	332	73.9	138	2 S21810	Ig heavy chain V r
23	331	73.7	246	2 S38950	Ig gamma chain - m
24	331	73.7	446	2 S40295	Ig gamma-2a chain
25	330.5	73.6	132	2 S46394	Ig heavy chain V r
26	330.5	73.6	137	2 H32513	Ig heavy chain pre
27	329.5	73.4	135	2 B32274	Ig heavy chain pre
28	329	73.3	127	2 S34014	Ig heavy chain V r
29	328.5	73.2	120	2 B22769	Ig heavy chain V r

ALIGNMENTS

RESULT 1

PH0961

Ig heavy chain V region (G6+ T-L33) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0961

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0961

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-119 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology <IMM>

F:31-35/Region: complementarity-determining 1

F:36-50/Region: complementarity-determining 2

F:51-67/Region: complementarity-determining 2

F:68-98/Region: framework 3

F:99-107/Region: complementarity-determining 3

Query Match 77.3%; Score 347; DB 2; Length 119;

Best Local Similarity 59.7%; Pred. No. 4.3e-27; Indels 32; Gaps 3;

Matches 71; Conservative 12; Mismatches 4;

QY 1 QIQLVQSGGVKPGASVRVSKASG-----YFTWVRQSPGKLEWI----- 43

Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTFFSSYALSWVRQAPGQGLEWMGGIPIFGTANY 60

QY 44 -----GKATLVDSKSTAYNELSLRSEDPAVYFCAR-----WGOGTTVTYSS 87

Db 61 AQKFGQRTIITADESTAYNELSLRSEDPAVYFCAR-----WGOGTTVTYSS 119

RESULT 2

PH0958

Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0958

R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.

J. Exp. Med. 175, 983-991, 1992

A:Title: Evidence for somatic selection of natural autoantibodies.

A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0958

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-122 <MAR>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-50/Region: framework 2
 F;51-67/Region: complementarity-determining 2
 F;68-98/Region: framework 3
 F;99-110/Region: complementarity-determining 3

Query Match 76.9%; Score 345.5; DB 2; Length 122;
 Best Local Similarity 58.2%; Pred. No. 6.2e-27;
 Matches 71; Conservative 12; Mismatches 4; Indels 35; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLWV----- 43
 DB 1 QVQLVQSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60
 QY 44 -----GKATLVTKSTSTAYMELSSLSRSEDVAVYFCAR-----WGQGTITVTV 85
 DB 61 AQKFGQGVITADESTSTAYMELSSLSRSEDVAVYFCARVNPFFAVGMDVWGQGTITVTV 120
 QY 86 SS 87
 DB 121 SS 122

RESULT 3

S36265
 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
 C;Accession: S36265
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36265; MUID:93178448; PMID:7679990
 A;Accession: S36265
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-118 <GRI>
 A;Cross-references: EMBL:Z18846; NID:G33121; PID:G939900
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 344.5; DB 2; Length 118;
 Best Local Similarity 61.0%; Pred. No. 7.6e-27;
 Matches 72; Conservative 9; Mismatches 6; Indels 31; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLWV----- 43
 DB 1 QVQLVQSGAEVKKPGASVKVSKASGYTPTGYMHVVRQAPGQGLEWMGWINPNSGGTNY 60
 QY 44 -----GKATLVTKSTSTAYMELSSLSRSEDVAVYFCAR-----WGQGTITVTV 87
 DB 61 AQKFGQGVITTRDTSASTAYMELSSLSRSEDVAVYFCARFLSGYLDVWGQGTITVTV 118

RESULT 4

PH0959
 Ig heavy chain V region (G6+ T-L26) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C;Accession: PH0959
 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A;Title: Evidence for somatic selection of natural autoantibodies.
 A;Reference number: PH0952; MUID:92202880; PMID:1552291
 A;Accession: PH0959
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-116 <MAR>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-50/Region: framework 2
 F;51-67/Region: complementarity-determining 2
 F;68-98/Region: framework 3
 F;99-104/Region: complementarity-determining 3

Query Match 76.3%; Score 342.5; DB 2; Length 116;
 Best Local Similarity 60.3%; Pred. No. 1.2e-26;
 Matches 70; Conservative 12; Mismatches 5; Indels 29; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLWV----- 43
 DB 1 QVQLVQSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60
 QY 44 -----GKATLVTKSTSTAYMELSSLSRSEDVAVYFCAR-----WGQGTITVTV 87
 DB 61 AQKFGQGVITADESTSTAYMELSSLSRSEDVAVYFCARNDWFDPMGQGTITVTV 116

RESULT 5

PH0960
 Ig heavy chain V region (G6+ T-L30) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C;Accession: PH0960
 R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A;Title: Evidence for somatic selection of natural autoantibodies.
 A;Reference number: PH0952; MUID:92202880; PMID:1552291
 A;Accession: PH0960
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-136 <MAR>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;1-30/Region: framework 1
 F;15-98/Domain: immunoglobulin homology <IMM>
 F;31-35/Region: complementarity-determining 1
 F;36-50/Region: framework 2
 F;51-67/Region: complementarity-determining 2
 F;68-98/Region: framework 3
 F;99-124/Region: complementarity-determining 3

Query Match 76.3%; Score 342.5; DB 2; Length 136;
 Best Local Similarity 52.9%; Pred. No. 1.4e-26;
 Matches 72; Conservative 11; Mismatches 4; Indels 49; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSKASG-----YSFTWRQSPGKGLWV----- 43
 DB 1 QVQLVQSGAEVKKPGSSVKVSKASGCTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60
 QY 44 -----GKATLVTKSTSTAYMELSSLSRSEDVAVYFCAR----- 76
 DB 61 AQKFGQGVITADKSTSTAYMELSSLSRSEDVAVYFCARTRVSVSTLYDSSGYDFSGY 120
 QY 77 -----WGQGTITVTVSS 87
 DB 121 YGMDVWGQGTITVTVSS 136

RESULT 6

A32483
 Ig heavy chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
 C;Accession: A32483
 R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C.
 Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
 A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us:
 A;Reference number: A32483; MUID:89273586; PMID:2499327

A:Accession: A32483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-142 <LAR>
 A:Cross-references: GB:M26463
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 341; DB 2; Length 142;
 Best Local Similarity 56.7%; Pred. No. 2e-26;
 Matches 72; Conservative 9; Mismatches 6; Indels 40; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASGVSFT-----YRQSPGKGLWMI----- 43
 DB 11 QVQLVQSGAEVKKPGASVKVSCKASGYTFNYMHVWVQAPGQGLEWMGIINPFGSTNY 70
 QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQG 80
 DB 71 AQKFGQGVITITADKSTSTAYMELSLRSEDVAVYFCAREKLTITGVLIITGMDYWGQ 130
 QY 81 TTVTVSS 87
 DB 131 TLTVSS 137

RESULT 7

PH0962
 Ig heavy chain V region (G6+ T-L42) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 A:Accession: PH0962
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880; PMID:1552291
 A:Accession: PH0962
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-120 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 120;
 Best Local Similarity 58.3%; Pred. No. 1.9e-26;
 Matches 70; Conservative 12; Mismatches 5; Indels 33; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWMI----- 43
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGIIPIFGTANY 60
 QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQGTITVSS 87
 DB 61 AQKFGQGVITITADKSTSTAYMELSLRSEDVAVYFCARGVAGPHFDYWGQGLTVTVSS 120

RESULT 8

PH0952
 Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 A:Accession: PH0952
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880; PMID:1552291

A:Accession: PH0952
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-128 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-116/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 128;
 Best Local Similarity 55.5%; Pred. No. 2e-26;
 Matches 71; Conservative 11; Mismatches 5; Indels 41; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWMI----- 43
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGIIPIFGTANY 60
 QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQ 79
 DB 61 AQKFGQGVITITADKSTSTAYMELSLRSEDVAVYFCARGGNYDIWGSYRNDADFIMGQ 120
 QY 80 GTTVTVSS 87
 DB 121 GIMTVTVSS 128

RESULT 9

PH0954
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 A:Accession: PH0954
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880; PMID:1552291
 A:Accession: PH0954
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-132 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-120/Region: complementarity-determining 3

Query Match 75.8%; Score 340.5; DB 2; Length 132;
 Best Local Similarity 53.8%; Pred. No. 2.1e-26;
 Matches 71; Conservative 12; Mismatches 4; Indels 45; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASG-----YSTWVRQSPGKGLWMI----- 43
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGGTFSSYALSWVRQAPGQGLEWMGIIPIFGTANY 60
 QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR----- 76
 DB 61 AQKFGQGVITITADKSTSTAYMELSLRSEDVAVYFCARPHASIDDFWISGYPNYYGMD 120
 QY 77 -WGQGTITVTVSS 87
 DB 121 VMQGTITVTVSS 132

RESULT 10

PH0955
IG heavy chain V region (G6+ CLL-AND) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0955
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kippes, T.J.
J. Exp. Med. 175, 993-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880; PMID:1552291
A:Accession: PH0955
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-30/Region: framework 1
F:31-35/Region: immunoglobulin homology <IMM>
F:36-50/Region: complementarity-determining 1
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-115/Region: complementarity-determining 3

Query Match 75.5%; Score 339; DB 2; Length 127;
Best Local Similarity 55.1%; Pred. No. 2.8e-26;
Matches 70; Conservative 13; Mismatches 4; Indels 40; Gaps 3;

Qy 1 QIQLVSGGVEKPKGASVRVSKASG-----YSFTWVRQSPGKGLEW----- 43
Db 1 QVQLVSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WSQG 80
Db 61 AQRFGQGVITADESTAYMELSSLRSEDTAVYCARVGVQVQHYIYNDVWGKG 120
Qy 81 TTVTVSS 87
Db 121 TTVTVSS 127

RESULT 11
C33548
IG heavy chain V-1 region (783) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: C33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression in the developing mouse.
A:Reference number: A33548; MUID:89345575; PMID:2503826
A:Accession: C33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-133 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 133;
Best Local Similarity 52.6%; Pred. No. 4.6e-26;
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVSGGVEKPKGASVRVSKASG-----YSFTWVRQSPGKGLEW----- 43
Db 1 QVQLVSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 60
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76
Db 61 AQRFGQGVITADESTAYMELSSLRSEDTAVYCAKTIILGYSSGWYPSNDYYVGM 120
Qy 77 --WGQGTITVTVSS 87

Db 121 DVMGQGTITVTVSS 133

RESULT 12
S14583
IG mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14583; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
A:Reference number: S14583; MUID:90332450; PMID:2115996
A:Accession: S14583
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:933451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.1%; Score 337; DB 2; Length 627;
Best Local Similarity 52.6%; Pred. No. 2.1e-25;
Matches 70; Conservative 13; Mismatches 4; Indels 46; Gaps 3;

Qy 1 QIQLVSGGVEKPKGASVRVSKASG-----YSFTWVRQSPGKGLEW----- 43
Db 20 QVQLVSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 79
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----- 76
Db 80 AQRFGQGVITADESTAYMELSSLRSEDTAVYCAKTIILGYSSGWYPSNDYYVGM 139
Qy 77 --WGQGTITVTVSS 87
Db 140 DVMGQGTITVTVSS 152

RESULT 13
A24672
IG heavy chain precursor V region (VMU-3.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C:Accession: A24672
R:Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A:Reference number: A91022; MUID:86055722; PMID:2998759
A:Accession: A24672
A:Molecule type: DNA
A:Residues: 1-119 <WIN>
A:Cross-references: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:g773576
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT>
F:18-101/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 119;
Best Local Similarity 60.3%; Pred. No. 4.6e-26;
Matches 70; Conservative 11; Mismatches 6; Indels 29; Gaps 3;

Qy 1 QIQLVSGGVEKPKGASVRVSKASGYSFT-----WVRQSPGKGLEW----- 43
Db 4 QVQLVSGAEVKKPGSSVKVSKASGDTFSSVAISWVRQAPGQGLEWMGGIPIFGTANY 63
Qy 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
Db 64 NGKFKGATLTADKSSSTAYMQLSSLTSEDSAVVFCARDYVGSYDWGQGTITVTVSS 119

RESULT 14

E33548
Ig heavy chain V-1 region (AND) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: B33548
R:Kippes, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expression
A:Reference number: A33548; MUID:99345575; PMID:2503826
A:Accession: B33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-126 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 126;
Best Local Similarity 55.6%; Pred. No. 4.9e-26;
Matches 70; Conservative 12; Mismatches 5; Indels 39; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASG-----YSFTWVRQSPGKGLEWI----- 43
Db 1 QVQLVQSGAEVKKPESVSVKVSKASGTFSSYALISWVRQAPGQGLEWMGIIIFGTANY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQGT 81
Db 61 AQKFGQGRVTITADESSTSTAYMELSLRSEDVAVYCARVSIFGVVQHYHYVMDVWGLGT 120
QY 82 TTVTVSS 87
Db 121 TTVTVSS 126

RESULT 15
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:Z46348; NID:G560839; PIDN:CAA86467.1; PID:G560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.9%; Score 336.5; DB 2; Length 135;
Best Local Similarity 60.3%; Pred. No. 5.2e-26;
Matches 70; Conservative 10; Mismatches 7; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSFT-----WVRQSPGKGLEWI----- 43
Db 20 QVQLVQSGAEVKKPGASVRSCKASGYTFGYMHWVRQAPGQGLEWMGWINPNSGGTNY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDVAVYFCAR-----WGQGTITVTVSS 87
Db 80 AQKFGQGRVTITADESSTSTAYMELSLRSDDTAVYCARATGYNVWQGTITVTVSS 135

Search completed: January 13, 2004, 12:44:41
Job time : 7.30655 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 / Search time 3.79913 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQLVQSGGVKKPGASVRV.....DTAVYFCARWGQTTTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326.5	72.7	139	1 HV07_MOUSE	P01751 mus musculu
2	322.5	71.8	137	1 HV11_MOUSE	P01755 mus musculu
3	320	71.3	117	1 HV12_MOUSE	P01756 mus musculu
4	320	71.3	117	1 HV13_MOUSE	P01757 mus musculu
5	313.5	69.8	118	1 HV11_MOUSE	P06330 mus musculu
6	310.5	69.2	147	1 HV1C_HUMAN	P01744 homo sapien
7	310	68.0	120	1 HV03_MOUSE	P01747 mus musculu
8	309.5	68.9	120	1 HV50_MOUSE	P06329 mus musculu
9	306	68.2	140	1 HV02_MOUSE	P01746 mus musculu
10	302	67.3	117	1 HV1B_HUMAN	P01743 homo sapien
11	302	67.3	138	1 HV48_MOUSE	P03980 mus musculu
12	296	65.9	121	1 HV01_MOUSE	P01745 mus musculu
13	295	65.7	117	1 HV1A_HUMAN	P01742 homo sapien
14	290.5	64.7	124	1 HV1D_HUMAN	P01760 homo sapien
15	289	64.4	117	1 HV1G_HUMAN	P23083 homo sapien
16	286	63.7	136	1 HV15_MOUSE	P01759 mus musculu
17	284	63.3	117	1 HV05_MOUSE	P01749 mus musculu
18	284	63.3	117	1 HV14_MOUSE	P01758 mus musculu
19	283	63.0	117	1 HV06_MOUSE	P01750 mus musculu
20	283	63.0	117	1 HV52_MOUSE	P06327 mus musculu
21	280	62.4	117	1 HV09_MOUSE	P01753 mus musculu
22	278	61.9	117	1 HV04_MOUSE	P01748 mus musculu
23	278	61.9	119	1 HV31_HUMAN	P01770 homo sapien
24	277.5	61.8	114	1 HV3B_HUMAN	P01763 homo sapien
25	277.5	61.8	124	1 HV1E_HUMAN	P01761 homo sapien
26	277	61.7	117	1 HV49_MOUSE	P06328 mus musculu
27	277	61.7	125	1 HV1F_HUMAN	P06326 homo sapien
28	276.5	61.6	114	1 HV00_MOUSE	P01741 mus musculu
29	276	61.5	117	1 HV10_MOUSE	P01754 mus musculu
30	276	61.5	121	1 HV3J_HUMAN	P01771 homo sapien
31	275.5	61.4	122	1 HV3G_HUMAN	P01768 homo sapien
32	271.5	60.5	116	1 HV3T_HUMAN	P01781 homo sapien
33	271.5	60.5	122	1 HV3H_HUMAN	P01769 homo sapien

ALIGNMENTS

RESULT 1

HV07_MOUSE STANDARD; PRT; 139 AA.

AC P01751; P01752; Rel. 01, Created
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RX MEDLINE=81234548; PubMed=6788376;

RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,

RA Baltimore D.;

RT "Heavy chain variable region contribution to the NPb family of

antibodies: somatic mutation evident in a gamma 2a variable region.";

RL Cell 24:625-637(1981).

CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA

MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL

(NPB ANTIBODIES).

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CC EMBL; J00529; AAA38170.1; -.

CC PIR; A90809; MHMS18.

CC PDB; 1AGU; 27-MAY-98.

CC PDB; 1AGW; 15-JUL-98.

CC InterPro; IPR007110; IG-like.

CC InterPro; IPR003086; IG_MHC.

CC InterPro; IPR003596; IG_V.

CC Pfam; PF00047; IG; 1.

CC SMART; SM00406; IGV; 1.

CC PROSITE; PS50835; IG LIKE; 1.

CC Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 19

FT CHAIN 20 139

FT DOMAIN 20 49 IG HEAVY CHAIN V REGION B1-8/186-2.

FT DOMAIN 50 54 FRAMEWORK-1.

FT DOMAIN 55 58 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 69 85 FRAMEWORK-2.

FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 118 124 D SEGMENT.

FT DOMAIN 125 139 CH2 SEGMENT.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 139 139

FT SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

SQ

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Query Match      72.7%; Score 325.5; DB 1; Length 139;
Best Local Similarity 56.7%; Pred. No. 1.1e-30;
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTTY 79

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTTY 79

QY 45 -----KALITVDKSTAYMELSLRSEDYAVFCAR-----WGQGTIVTVSS 87
DB 80 NEHFRSKATLTIDKPSSTAYMQLSSITSDSAVYCYARYLGRFYDWGQGTITLVSS 137

RESULT 2
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.; variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137
FT SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match      71.8%; Score 322.5; DB 1; Length 137;
Best Local Similarity 56.8%; Pred. No. 3.1e-30;
Matches 67; Conservative 11; Mismatches 9; Indels 31; Gaps 3;

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QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 20 QVQLQQPGAEVFKPGASVKLSCKASGYTFTSYLHMWVNRQPGKGLWIGRIDPNSGGTTY 79

QY 45 -----KALITVDKSTAYMELSLRSEDYAVFCAR-----WGQGTIVTVSS 87
DB 80 NEHFRSKATLTIDKPSSTAYMQLSSITSDSAVYCYARYLGRFYDWGQGTITLVSS 137

RESULT 3
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02039; MMS4E.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Glycoprotein.
KW Immunoglobulin V region; IG-LIKE.
FT DOMAIN 1 116
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON TER 117
FT SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match      71.3%; Score 320; DB 1; Length 117;
Best Local Similarity 59.1%; Pred. No. 5.1e-30;
Matches 68; Conservative 12; Mismatches 7; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 43
DB 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWKVQSHGKSLWIGIDNPNGGTSY 60

QY 44 -----GXATITVDKSTAYMELSLRSEDYAVFCAR-----WGQGTIVTVSS 87
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDYAVYCYARDYDWYFWGAGTIVTVSS 117

RESULT 4
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

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RN SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RL rearrangements in heavy chain V-region gene segments.";
RT Nature 283:35-40(1980)
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS. MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A26242; MEMS75.
DR HSSP: P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 71.3%; Score 320; DB 1; Length 117;
Best Local Similarity 58.1%; Pred. No. 5.1e-30; Indels 30; Gaps 3;
Matches 68; Conservative 12; Mismatches 7;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYMKWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYNELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCYRDYVYFDVWGAGTITVTVSS 117

RESULT 5
HV51 MOUSE
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR: A02040; MEMS38.
DR HSSP: P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

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Query Match 69.8%; Score 313.5; DB 1; Length 118;
Best Local Similarity 56.8%; Pred. No. 2.9e-29; Indels 31; Gaps 3;
Matches 67; Conservative 10; Mismatches 10;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYMKWVKQSHGKSLWIGDINPNNGTSTY 60
QY 44 -----GKATLTVDKSTSTAYNELSLRSEDATVYFCAR-----WGQGTITVTVSS 87
DB 61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCYRDYVYFDVWGAGTITVTVSS 118

RESULT 6
HV1C HUMAN
ID HV1C HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; 1MCP.
DR GO; GO:000576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948P9F72A5366C20 CRC64;

Query Match 69.2%; Score 310.5; DB 1; Length 147;
Best Local Similarity 50.8%; Pred. No. 8.2e-29; Indels 41; Gaps 3;
Matches 65; Conservative 13; Mismatches 9;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWEI----- 43
DB 20 QTQLVQSGAEVRKPGASVRVSKASGYTFIDSYIHWIQAPGHGKLEWVGNPNPNSGGTNY 79

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QY 44 -----GKATLVKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 80 APRQGRVMTDRASPSTAYMDLSRLSDSAVFCARSDPFWSDYFNDYSYTLTDWGO 139
QY 80 GTTIVTSS 87
DB 140 GTTIVTSS 147

RESULT 7
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of the strain A mouse.";
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; PF04E4A167B654AF CRC64;

Query Match 69.0%; Score 310; DB 1; Length 120;
Best Local Similarity 54.2%; Pred. No. 7.5e-29;
Matches 65; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

QY 2 IQLVQSGEVKPKGASVRUSCKASGYSTFT-----WVRQSPGKLEWI-----43
DB 1 VQLQSGAEVLVRAGSSVVKSCASGYSTFTSYGYNWVKRPPGQGLEWIGVINGVTKYN 60
QY 44 -----GKATLVKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 61 EKFGKGTLLTVDKSSSTAYMQLSLRSDSAVFCARSVYGGSYFVYMGQTTLVSS 120

RESULT 8
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8313846; PubMed=6186498;
RA Siekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of the strain A mouse.";
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; PF04E4A167B654AF CRC64;

Query Match 69.0%; Score 310; DB 1; Length 120;
Best Local Similarity 54.2%; Pred. No. 7.5e-29;
Matches 65; Conservative 13; Mismatches 8; Indels 34; Gaps 3;

QY 2 IQLVQSGEVKPKGASVRUSCKASGYSTFT-----WVRQSPGKLEWI-----43
DB 1 VQLQSGAEVLVRAGSSVVKSCASGYSTFTSYGYNWVKRPPGQGLEWIGVINGVTKYN 60
QY 44 -----GKATLVKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 61 EKFGKGTLLTVDKSSSTAYMQLSLRSDSAVFCARSVYGGSYFVYMGQTTLVSS 120

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; --
CC PIR; A94264; HVM5G7.
CC HSP; P01810; 2EBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
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```
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Borens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RA "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MEMS15.
DR HSP; P01810; 2EBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 68.9%; Score 309.5; DB 1; Length 120;
Best Local Similarity 54.3%; Pred. No. 8.5e-29;
Matches 65; Conservative 12; Mismatches 10; Indels 33; Gaps 3;

QY 1 QIQLVQSGEVKPKGASVRUSCKASGYSTFT-----WVRQSPGKLEWIG-----44
DB 1 QVQLQGLPQELVLPKASVNLSCASGYSTFTSYGMHWIRORPGQGLEWIGINFSNGTNY 60
QY 45 -----KATLVKSTAYMELSLRSEDVAVFCAR-----WGO 79
DB 61 NEKFKSATLVKSSSATYMQLTSTPSEDSAVYCARWDYEGDRYFDVNGTGTIVTSS 120

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estes P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; J00493; AAA38128.1; --
CC PIR; A94264; HVM5G7.
CC HSP; P01810; 2EBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
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DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 93G7.
FT CHAIN 20 140 IG-LIKE.
FT DOMAIN 20 139
FT NON_TER 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C88 CRC64;

Query Match
Best Local Similarity 68.2%; Score 306; DB 1; Length 140;
Matches 64; Conservative 14; Mismatches 9; Indels 34; Gaps 3;

QY 1 QIQLVSGGEVKPGASVRSCKASGYSFT-----WYRQSPGKLEWI----- 43
DB 20 EVQLQQSGAEIVRAGSSVYMSCKASGYSFTSYNGYNWYKQRPQGLEGWIGYINPENGVIYNY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSRSEDVAVYFCAR-----WQGGTTVTVS 86
DB 80 NEKFKGKTLTVDKSSSTAYMQLSLTSEDSAVYFCARSHYGGSYDFDYWGQGTPLTVS 139
QY 87 S 87
DB 140 S 140

RESULT 10
HVB_HUMAN
ID HVB_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region H3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Glivol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC6C0CD1FE7 CRC64;

Query Match
Best Local Similarity 67.3%; Score 302; DB 1; Length 117;
Matches 61; Conservative 9; Mismatches 6; Indels 22; Gaps 2;

QY 1 QIQLVSGGEVKPGASVRSCKASGYSFT-----WYRQSPGKLEWI----- 43
DB 20 QVQLVSGAEIVKPGASVRSCKASGYSFTSYNFMWVFRQAPQGLEGWIGIINPNSGGSYSY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSRSEDVAVYFCAR 76
DB 80 AQKFGQRTVIRDTSTVYMWELSLRSRSEDVAVYCAR 117

RESULT 11
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03950;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F., Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR FIR; A02033; HVMS77.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match
Best Local Similarity 67.3%; Score 302; DB 1; Length 138;
Matches 64; Conservative 13; Mismatches 10; Indels 32; Gaps 3;

QY 1 QIQLVSGGEVKPGASVRSCKASGYSFT-----WYRQSPGKLEWI----- 44
DB 20 QVQLQQSGAEIVKPGASVRSCKASGYSFTSYNFMWVFRQAPQGLEGWIGIINPNSGGSYSY 79
QY 45 -----KATLTVDKSTSTAYMELSLRSRSEDVAVYFCAR-----WQGGTTVTVS 87
DB 80 NEKFKKATLTVDKSSSTAYMQLSLTPEBFAVYCARSDGYDFVYWGQGTPLTVSA 138

RESULT 12
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;

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DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 region of immunoglobulin heavy chain MPC11.";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
 FROM A MYELOMA THAT SECRETES IGG2B.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A93708; GWS11.
 DR HSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 FT DOMAIN 1 112 IG-LIKE.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

 Query Match 65.9%; Score 296; DB 1; Length 121;
 Best Local Similarity 50.4%; Pred. No. 3.1e-27;
 Matches 61; Conservative 15; Mismatches 11; Indels 34; Gaps 3;

 QY 1 QIQLVSGGEVKPGASVRVSCASGYST-----WVROSPGKGLWV----- 43
 Db 1 EAQLQSGAEVLPVPGTSVKISCAAGYTFYTWIGWKPGRGGLWIGDIYPPGGFTNY 60

 QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WQGGTITVTS 86
 Db 61 NDNLKGKATLTATSTSSYAIQLSSLTSDSAIYHCARGIYNSPYFDSWQGTITLVS 120

 QY 87 S 87
 Db 121 S 121

 RESULT 13
 HVID HUMAN STANDARD; PRT; 117 AA.
 ID HVID_HUMAN
 AC P01742;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region EU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71064024; PubMed=5489771;
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RA Waxdal M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 acid sequence of heavy-chain bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170(1970).
 RN [2]

RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3189-3196(1970).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
 MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A90563; GIHUEU.
 DR HSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 DR Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 22 96
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAE8B52818 CRC64;

 Query Match 65.7%; Score 295; DB 1; Length 117;
 Best Local Similarity 55.6%; Pred. No. 3.9e-27;
 Matches 65; Conservative 13; Mismatches 9; Indels 30; Gaps 4;

 QY 1 QIQLVSGGEVKPGASVRVSCASGYST-----WVROSPGKGLWV----- 43
 Db 1 QVQLVQSGAEVKKPGSSVKVSCASGCTFERSAIIVWRQAPGGLEWMGIVPMFGPPNY 60

 QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----QQTITVTS 87
 Db 61 AQKFGQGVTTTADSTWYMWELSSLRSEDTAVYFCAGGYVSPSEYNGGLVTS 117

 RESULT 14
 HVID HUMAN STANDARD; PRT; 124 AA.
 ID HVID_HUMAN
 AC P01760;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region WOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82046599; PubMed=7028111;
 RA Andrews D.W., Capra J.D.;
 RT "Amino acid sequence of the variable regions of heavy chains from two
 RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 group.";
 RL Biochemistry 20:5822-5830(1981).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 GLOBULIN ACTIVITY.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02043; M1HUL.
 DR HSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
 FT DOMAIN 1 112 IG-LIKE.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON-TER 124 124
 SQ SEQUENCE 124 AA; 13684 MW; CB98F365D004EC8B CRC64;

Query Match 64.7%; Score 290.5; DB 1; Length 124;
 Best Local Similarity 50.8%; Pred. No. 1.4e-26;
 Matches 62; Conservative 14; Mismatches 11; Indels 35; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WYRQSPGKGLWIG-----44
 DB 1 QVQLMQSGAEVKKPGASVRVSCKASGYSTFTDYKGLWVRQAPGKGLWVGQIPIRPFNGEVK 60
 QY 45 -----KATLTVDKSTSTAYMELSSLSRSEDVAVYFCAR-----WCQGTITVTV 85
 DB 61 NPGSVRVSVSLKFSFQAHEMLSSLSRSEDVAVYFCAREYGFDTSDYVYYVWGQGLTVTV 120
 QY 86 SS 87
 DB 121 SS 122

RESULT 15

HV1G_HUMAN STANDARD; PRT; 117 AA.
 AC P23083;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 heavy-chain locus."
 RL EMBO J. 7:1047-1051(1988).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X07448; -; NOT ANNOTATED_CDS.
 DR PIR; S00476; HVHU35.
 DR HSP; P01772; 2FE4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal.
 SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON-TER 117 117
 SQ SEQUENCE 117 AA; 13009 MW; BB61CE63F8CB97BD CRC64;

Query Match 64.4%; Score 289; DB 1; Length 117;
 Best Local Similarity 60.2%; Pred. No. 1.9e-26;
 Matches 59; Conservative 9; Mismatches 8; Indels 22; Gaps 2;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WYRQSPGKGLWIG-----43
 DB 20 QVQLVQSGAEVKKPGASVRVSCKASGYSTFTGYVYHWRQAPGQGLWNGRINPNSGGTNY 79
 QY 44 -----GKATLTVDKSTSTAYMELSSLSRSEDVAVYFCAR 76
 DB 80 AQKFGQRTVSTRDTSISTAYMELSLRLSRSDDTVYVYCAR 117

Search completed: January 13, 2004, 12:39:26
 Job time : 3.79913 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 15.5764 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 Q1QLVSGGEVKKPGASVRV.....DTAVFCARWGQTTVTWSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258032604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_23.*

2: sp_archaea.*

3: sp_bacteria.*

4: sp_fungi.*

5: sp_human.*

6: sp_invertebrate.*

7: sp_mammal.*

8: sp_mhc.*

9: sp_organelle.*

10: sp_phage.*

11: sp_plant.*

12: sp_rodent.*

13: sp_virus.*

14: sp_vertebrate.*

15: sp_unclassified.*

16: sp_rvirus.*

17: sp_bacteriap.*

18: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337	75.1	119	5 Q9GYZ2	Q9GYZ2 schistosoma
2	333	74.2	119	4 Q9UL94	Q9UL94 homo sapien
3	332.5	74.1	124	4 Q9UL92	Q9UL92 homo sapien
4	331	73.7	473	11 Q9D8L4	Q9D8L4 mus musculu
5	330.5	73.6	137	11 Q924R6	Q924R6 mus musculu
6	330.5	73.6	159	4 Q9EQS0	Q9EQS0 homo sapien
7	329	73.3	142	11 Q924Q1	Q924Q1 mus musculu
8	328.5	73.2	141	11 Q924Q4	Q924Q4 mus musculu
9	328	73.1	140	11 Q924R2	Q924R2 mus musculu
10	326.5	72.7	143	11 Q924R0	Q924R0 mus musculu
11	326.5	72.7	145	11 Q924Q7	Q924Q7 mus musculu
12	326	72.6	146	11 Q924R8	Q924R8 mus musculu
13	326	72.6	146	11 Q924Q8	Q924Q8 mus musculu
14	325.5	72.5	145	11 Q924Q6	Q924Q6 mus musculu
15	325.5	72.5	145	11 Q924Q9	Q924Q9 mus musculu
16	325.5	72.5	145	11 Q924R1	Q924R1 mus musculu

17	325.5	72.5	145	11 Q924R4	Q924R4 mus musculu
18	325	72.4	146	11 Q924Q3	Q924Q3 mus musculu
19	324.5	72.3	143	11 Q924Q5	Q924Q5 mus musculu
20	323.5	72.0	145	11 Q924R3	Q924R3 mus musculu
21	323	71.9	117	11 Q9QXF0	Q9QXF0 mus musculu
22	323	71.9	125	4 Q9UL95	Q9UL95 homo sapien
23	322.5	71.8	482	11 Q8K172	Q8K172 mus musculu
24	322	71.7	117	11 Q9QX89	Q9QX89 mus musculu
25	321.5	71.6	143	11 Q924R7	Q924R7 mus musculu
26	320	71.3	147	11 Q925S3	Q925S3 mus musculu
27	320	71.3	614	4 Q96GA6	Q96GA6 homo sapien
28	319.5	71.2	143	11 Q924Q0	Q924Q0 mus musculu
29	319.5	71.2	145	11 Q924P7	Q924P7 mus musculu
30	319	71.0	150	4 Q9Y298	Q9Y298 homo sapien
31	319	71.0	481	11 Q91W11	Q91W11 mus musculu
32	318.5	70.9	143	11 Q924P9	Q924P9 mus musculu
33	318.5	70.9	463	11 Q991C4	Q991C4 mus musculu
34	318	70.8	142	11 Q924Q2	Q924Q2 mus musculu
35	318	70.8	144	11 Q924P5	Q924P5 mus musculu
36	317.5	70.7	116	4 Q9UL89	Q9UL89 homo sapien
37	316.5	70.5	143	11 Q91VA2	Q91VA2 mus musculu
38	316.5	70.5	500	4 Q9BRV0	Q9BRV0 homo sapien
39	316	70.4	140	11 Q924P8	Q924P8 mus musculu
40	315.5	70.3	143	11 Q924P6	Q924P6 mus musculu
41	314.5	70.0	118	11 Q921C4	Q921C4 mus musculu
42	314	69.9	120	11 Q920E8	Q920E8 mus musculu
43	314	69.9	123	11 Q8VLJ1	Q8VLJ1 mus musculu
44	313.5	69.8	139	11 Q924R5	Q924R5 mus musculu
45	310.5	69.2	613	11 Q8VCX7	Q8VCX7 mus musculu

ALIGNMENTS

RESULT 1

Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2; DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Monoclonal anti-idiotypic antibody NP30 heavy chain variable region (fragment).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1;
DR HSSP; P01772; 2FE4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA93873FD5FA6AB CRC64;

Query Match 75.1%; Score 337; DB 5; Length 119;

Best Local Similarity 58.8%; Pred. No. 1.3e-30;

Matches 70; Conservative 10; Mismatches 7; Indels 32; Gaps 3;

QY 1 Q1QLVSGGEVKKPGASVRVSCKASGYFT-----WYQSPKGLGWIG----- 44

DB 1 QVQLVESGAEVRKPGASVRVSCKASGYFTTGTGYMNVWRQAPGHGIEWIGINPSRGYTNV 60

QY 45 -----KATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 87
Db 61 NQKFKDRTVTMTKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 119

RESULT 2
Q9UL94
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035020; AAD56258.1; -
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345P4A16E CRC64;

Query Match 74.2%; Score 333; DB 4; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.8e-30;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

QY 1 QIQLVQSGGVEKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----43
Db 1 EVQLVESGAEVKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 87
Db 61 AQKFGKVTMTKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 119

RESULT 3
Q9UL92
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035020; AAD56258.1; -
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345P4A16E CRC64;

Query Match 74.2%; Score 333; DB 4; Length 119;
Best Local Similarity 58.0%; Pred. No. 3.8e-30;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

QY 1 QIQLVQSGGVEKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----43
Db 1 EVQLVESGAEVKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 87
Db 61 AQKFGKVTMTKSTAYMELSLRSRSDTAVYFCAR-----WGQTTVTSS 119

EMBL; AF035022; AAD56258.1; -
DR HSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 124
SQ SEQUENCE 124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;

Query Match 74.1%; Score 332.5; DB 4; Length 124;
Best Local Similarity 55.6%; Pred. No. 4.8e-30;
Matches 69; Conservative 12; Mismatches 6; Indels 37; Gaps 3;

QY 1 QIQLVQSGGVEKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----43
Db 1 EVQLVESGAEVKPKGASVYRSCASGYSTF-----WVRSQSPGKLEWI-----60

QY 44 -----GKATLTVDKSTAYMELSLRSRSDTAVYFCAR-----WGQTTV 83
Db 61 AQKFGKVTMTKSTAYMELSLRSRSDTAVYFCAR-----WGQTTV 120

QY 84 TVSS 87
Db 121 TVSS 124

RESULT 4
Q9DL84
ID Q9DL84 PRELIMINARY; PRT; 473 AA.
AC Q9DL84
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE 181006009Rik protein.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Saito T., Okazaki Y., Gojohori T., Sono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
RA Watanabe-Borisi A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.

```
DR SMART, SMO0406; IGV, 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 1.
SQ SEQUENCE 473 AA; 5:699 MW; 9DED57A514475PBB CRC64;

Query Match
Best Local Similarity 58.0%; Score 331; DB 11; Length 473;
Matches 69; Conservative 11; Mismatches 7; Indels 32; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWV----- 43
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLVQSGAEVKKPGASVKISCKASGYTFDYINWVKRPGQGLEWIKIGPGSGSTVY 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 NEXFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARSDYDWFAYWGQGTITVTVSA 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
Q924R6 PRELIMINARY; PRT; 137 AA.
ID Q924R6
AC Q924R6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186 2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;

Query Match
Best Local Similarity 73.6%; Score 330.5; DB 11; Length 137;
Matches 70; Conservative 11; Mismatches 6; Indels 43; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWV----- 43
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLVQSGAEVKKPGASVKYSCASGYTFSNYMNWVRQPGQPEWGVINPSGGGARY 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----W 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 SQKFGRLTWTRDTSTSTVYMDLSSLRSDTAVYFCAREMEITFGGAVSKGFYYGMDVW 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
Q96QSO PRELIMINARY; PRT; 159 AA.
ID Q96QSO
AC Q96QSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match
Best Local Similarity 60.7%; Score 330.5; DB 11; Length 137;
Matches 68; Conservative 12; Mismatches 7; Indels 25; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWIG----- 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLQPGAEVKKPGASVKLSCKASGYTFSTYVWVWVKRPGQGLEWIGRIDPNSGGTKY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 45 -----KATLTVDKSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVTVSS 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 NEXFKGKATLTVDKPSSTAYMQLSSLTSDSAVYFCARWDYWGQGTITVTVSS 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
ID Q924Q1
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;

Query Match
Best Local Similarity 73.3%; Score 329; DB 11; Length 142;
Matches 69; Conservative 12; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWIG----- 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLQPGTELVKKPGASVKLSCKASGYTFSTYVWVWVKRPGQGLEWIGINPNSGGTNY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
   Tilson M.D.;
RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF00047; Ig_v.
DR SMART; SMO0406; IGV, 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match
Best Local Similarity 53.8%; Score 330.5; DB 4; Length 159;
Matches 70; Conservative 11; Mismatches 6; Indels 43; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWV----- 43
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 20 QVQLVQSGAEVKKPGASVKYSCASGYTFSNYMNWVRQPGQPEWGVINPSGGGARY 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 44 -----GKATLTVDKSTAYMELSSLRSEDTAVYFCAR-----W 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 SQKFGRLTWTRDTSTSTVYMDLSSLRSDTAVYFCAREMEITFGGAVSKGFYYGMDVW 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
ID Q924Q1
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;

Query Match
Best Local Similarity 59.0%; Score 329; DB 11; Length 142;
Matches 69; Conservative 12; Mismatches 6; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRSCKASGYSTF-----WVRSQPGKGLWIG----- 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLQPGTELVKKPGASVKLSCKASGYTFSTYVWVWVKRPGQGLEWIGINPNSGGTNY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDYAVYFCAR-----WGQGTITVTYSS 87
DB 61 NEKFKSKATLTVDKSSSTAYMQLSLTSDSAVYICARWEADYWGQGTITVTYSS 117

RESULT 8
Q924Q4 PRELIMINARY; PRT; 141 AA.
AC Q924Q4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067796; BAB63281.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 73.2%; Score 328.5; DB 11; Length 141;
Best Local Similarity 58.6%; Pred. No. 1.5e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 29; Gaps 3;

QY 1 QIQLVSGGEVKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDYAVYFCAR-----WGQGTITVTYSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICARDYGRTFWGQGTITVTYSS 116

RESULT 9
Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067798; BAB63273.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 72.7%; Score 326.5; DB 11; Length 143;
Best Local Similarity 57.6%; Pred. No. 2.6e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 31; Gaps 3;

QY 1 QIQLVSGGEVKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDYAVYFCAR-----WGQGTITVTYSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICARWDEYAMDYWGQGTITVTYSS 118

RESULT 11
Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
```

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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 73.1%; Score 328; DB 11; Length 140;
Best Local Similarity 59.1%; Pred. No. 1.7e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 28; Gaps 3;

QY 1 QIQLVSGGEVKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDYAVYFCAR-----WGQGTITVTYSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICARYAGDYWGQGTITVTYSS 115

RESULT 10
Q924R0 PRELIMINARY; PRT; 143 AA.
AC Q924R0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067790; BAB63275.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match 72.7%; Score 326.5; DB 11; Length 143;
Best Local Similarity 57.6%; Pred. No. 2.6e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 31; Gaps 3;

QY 1 QIQLVSGGEVKPGASRVSCASGYST-----WVROSPGKLEWIG----- 44
DB 1 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYNMHWVKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSEDYAVYFCAR-----WGQGTITVTYSS 87
DB 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYICARWDEYAMDYWGQGTITVTYSS 118

RESULT 11
Q924Q7 PRELIMINARY; PRT; 145 AA.
AC Q924Q7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003006; IG-MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 72.6%; Score 326.5; DB 11; Length 145;
Best Local Similarity 56.7%; Pred. No. 2.7e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 1 QVQLQQPQAEIVKPGASVKLSCKASGTFSTSYMMHWYKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 87
DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPDYWGQGTITVTVSS 120

RESULT 12
Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067781; BAB63266.1; -
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003006; IG-MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;

Query Match 72.6%; Score 326; DB 11; Length 145;
Best Local Similarity 56.2%; Pred. No. 3.1e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 34; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 1 QVQLQQPQAEIVKPGASVKLSCKASGTFSTSYMMHWYKQRPGRGLEWIGRIDPNSGGTKY 60

QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 86
DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPDYWGQGTITVTVSS 120
QY 87 S 87
DB 121 S 121
RESULT 13
Q924Q8 PRELIMINARY; PRT; 146 AA.
AC Q924Q8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067792; BAB63277.1; -
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003006; IG-MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16023 MW; 4B04959991D49159 CRC64;

Query Match 72.6%; Score 326; DB 11; Length 146;
Best Local Similarity 56.2%; Pred. No. 3.1e-29;
Matches 68; Conservative 12; Mismatches 7; Indels 34; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFT-----WVRQSPGKGLWIG----- 44
DB 1 QVQLQQPQAEIVKPGASVKLSCKASGTFSTSYMMHWYKQRPGRGLEWIGRIDPNSGGTKY 60
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 86
DB 61 NEKPKSKATLTVDKPSSTAYMQLSLTSEDSAVYVCARTFTTIVVAPDYWGQGTITVTVSS 120
QY 87 S 87
DB 121 S 121

RESULT 14
Q924Q6 PRELIMINARY; PRT; 145 AA.
AC Q924Q6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;

Search completed: January 13, 2004, 12:43:07
Job time : 16.5764 secs

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RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RL Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
DR EMBL; AB067794; BAB63279.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_V.  
DR Pfam; PF00047; Ig_1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON_TER 1  
FT NON_TER 145  
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;  
  
Query Match 72.5%; Score 325.5; DB 11; Length 145;  
Best Local Similarity 56.7%; Pred. No. 3.5e-29;  
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYFT-----WVRQSPGKGLEWIG----- 44  
Db 1 QVQLQPGAEVLPKPGASVKLSCKASGYFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAYFCAR-----WGQGTITVTVSS 87  
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYIYANDYWGQGTITVTVSS 120  
  
RESULT 15  
Q924Q9 PRELIMINARY; PRT; 145 AA.  
AC Q924Q9;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE VH186.2-D-J-C mu protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RA Kozono Y., Kozono H., Azuma T.;  
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals  
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-  
RL Hydroxy-3-Nitrophenyl)Acetyl (NP).";  
DR EMBL; AB067791; BAB63276.1; -  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_V.  
DR Pfam; PF00047; Ig_1.  
DR SMART; SMC0406; IGV; 1.  
DR PROSITE; PSS0835; IG_LIKE; 1.  
FT NON_TER 1  
FT NON_TER 145  
SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;  
  
Query Match 72.5%; Score 325.5; DB 11; Length 145;  
Best Local Similarity 56.7%; Pred. No. 3.5e-29;  
Matches 68; Conservative 12; Mismatches 7; Indels 33; Gaps 3;  
  
QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYFT-----WVRQSPGKGLEWIG----- 44  
Db 1 QVQLQPGAEVLPKPGASVKLSCKASGYFTSYMHVWVKQRPGRGLEWIGRIDPNSGGTKY 60  
QY 45 -----KATLTVDKSTSTAYMELSLRSEDYAYFCAR-----WGQGTITVTVSS 87  
Db 61 NEKFKSKATLTVDKPSSTAYMQLSLTSDSAVYCARSTLSHYIYANDYWGQGTITVTVSS 120
```


PR 30-JUN-1994; 94CU-0000080.
 XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 PA Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
 XX WPI; 1996-130770/14.
 XX
 XX Identifying interspecies differences in amino acid sequence of Ig
 PT T-cell epitopes - by sequence comparison, also humanised antibodies
 PT contg. altered T-cell epitopes, retaining antigen specificity but
 PT not immunogenicity, esp. for tumour treatment
 XX
 XX Claim 14; Fig 2; 33pp; English.
 XX
 XX The sequence represents residues from a human immunoglobulin with
 CC homology to the heavy chain variable region of monoclonal antibody
 CC IOR-R3 (AAR2990), specific for epidermal growth factor receptor,
 CC produced by a mouse hybridoma. The sequence is partial, and
 CC complementarity determining regions are omitted. The sequence is
 CC isolated by comparison of human and mouse immunoglobulins and
 CC analysis for T-lymphocyte antigenic sequences using a computer
 CC algorithm. Residues not within a complementarity determining region,
 CC canonical structure or Verner zone may be modified to reduce
 CC immunogenicity in humans (e.g. in sequence AAR2992). This method,
 CC which involves the introduction of only a few point mutations into
 CC T-cell epitope coding regions, is generally applicable in humanisation
 CC of mouse antibodies. The resulting humanised antibodies may be used
 CC e.g. as antitumour agents. They retain the antigen recognition of the
 CC original antibody, but are not immunogenic in humans.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 87 AA;
 SQ
 Query Match 86.0%; Score 386; DB 17; Length 87;
 Best Local Similarity 81.6%; Pred. No. 3.9e-29;
 Matches 71; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QIQLVQSGGEVKKPGASVRSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFNWRQAPGQGLEWMGRVTRDTSSTAYME 60
 QY 61 LSSLRSEDTAVYFCARWGQGTFTVSS 87
 DB 61 LSSLRSEDTAVYFCARWGQGTFTVSS 87
 RESULT 2
 ID ABG74721 standard; Protein; 87 AA.
 XX
 XX ABG74721;
 XX
 XX 10-MAY-2003 (first entry)
 XX
 XX Murine humanised Mu007-associated protein DP-5.
 DE
 XX Murine; light chain; variable region; antibody; Crohn's disease;
 KW human interleukin (IL)-1beta; antirheumatic; antiarthritic; humanised;
 KW antiinflammatory; osteopathic; antiallergic; cerebroprotective;
 KW antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007;
 KW rheumatoid arthritis; osteoarthritis; cartilage destruction;
 KW allergy; septic shock; endotoxemia; stroke; asthma;
 KW graft versus host disease; inflammatory bowel disease; DP-5.
 XX
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 XX Region 26..30
 XX FT /note= "Amino acid involved in tertiary structure"
 XX PN WO2003010282-A2.
 XX
 XX 06-FEB-2003.
 XX
 XX 18-JUL-2002; 2002WO-US21281.
 XX
 XX

PR 26-JUL-2001; 2001US-307973P.
 XX 14-AUG-2001; 2001US-312278P.
 PA (ELIL) LILLY & CO ELI.
 XX Bright SW, Jia AY, Kuhstoss SA, Manetta JV, Tsurushita N;
 PI Vasquez MJ;
 XX WPI; 2003-248068/24.
 XX
 XX New IL-1beta antibodies, useful for treating allergy, septic or
 PT endotoxic shock, septicemia, stroke, asthma, graft versus host disease,
 PT Crohn's disease, or inflammatory bowel disease -
 XX
 XX Disclosure; Fig 2; 98pp; English.
 XX
 XX This invention describes a novel antibody that specifically binds mature
 CC human interleukin (IL)-1beta, and binds the same epitope on mature human
 CC IL-1beta as mouse monoclonal antibody Mu007 or humanized antibody Hu007.
 CC The antibody of the invention have antirheumatic, antiarthritic,
 CC antiinflammatory, osteopathic, antiallergic, cerebroprotective,
 CC antiasthmatic, immunosuppressive and antibacterial activity and can be
 CC used in a vaccine. The antibody is useful for manufacturing a medicament
 CC for treating rheumatoid arthritis or osteoarthritis, or for inhibiting
 CC cartilage destruction in a subject. The antibody is also useful for
 CC treating allergy, septic or endotoxic shock, septicemia, stroke, asthma,
 CC graft versus host disease, Crohn's disease, or inflammatory bowel
 CC disease. This sequence represents a protein associated with the
 CC humanised murine Mu007 antibody described in the disclosure of the
 XX invention.
 XX
 XX Sequence 87 AA;
 SQ
 Query Match 84.6%; Score 380; DB 24; Length 87;
 Best Local Similarity 80.5%; Pred. No. 1.4e-28;
 Matches 70; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 1 QIQLVQSGGEVKKPGASVRSCKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKYSGYTLTWVRQAPGKGLWNGRVTMTEDTSTDTAYME 60
 QY 61 LSSLRSEDTAVYFCARWGQGTFTVSS 87
 DB 61 LSSLRSEDTAVYFCARWGQGTFTVSS 87
 RESULT 3
 AAR93003
 ID AAR93003 standard; Protein; 87 AA.
 XX
 XX AAR93003;
 XX
 XX 25-MAR-2003 (updated)
 DT 18-MAY-1996 (first entry)
 XX
 XX Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.
 DE
 XX IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology;
 KW variable region; framework; cloning; computer; algorithm;
 KW immunogenicity; site-directed mutagenesis; T-lymphocyte epitope;
 KW tertiary structure; point mutation; antibody engineering;
 KW protein engineering; humanised antibody; antitumour; cancer; therapy.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 XX Region 26..30
 XX FT /note= "Amino acid involved in tertiary structure"
 XX FT Region 50
 XX FT /note= "Amino acid involved in tertiary structure"
 XX FT Region 76
 XX FT /note= "Amino acid involved in tertiary structure"
 XX

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FN EP699755-A2.
XX
PD 06-MAR-1996.
XX
PF 27-JUN-1995; 95EP-0201752.
XX
PR 30-JUN-1994; 94CU-0000080.
XX
PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX
DR WPI; 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig
XX T-cell epitopes - by sequence comparison, also humanised antibodies
XX contg. altered T-cell epitopes, retaining antigen specificity but
XX not immunogenicity, esp. for tumour treatment
XX
XX Claim 22; Fig 9; 33pp; English.
XX
XX The sequence represents residues from a human immunoglobulin with
XX homology to the heavy chain variable region from mouse monoclonal
XX antibody IOR-CEA-1 (AA93002). The sequence is partial, and
XX complementarity determining regions are omitted. The sequence is
XX isolated by comparison of human and mouse immunoglobulins and
XX analysis for T-lymphocyte antigenic sequences using a computer
XX algorithm. Residues not within a complementarity determining region,
XX canonical structure or Vernier zone may be modified to reduce
XX immunogenicity in humans (e.g. in sequence AA93004). This method,
XX which involves the introduction of only a few point mutations into
XX T-cell epitope coding regions, is generally applicable in humanisation
XX of mouse antibodies. The resulting humanised antibodies may be used
XX e.g. as antitumour agents. They retain the antigen recognition of the
XX original antibody, but are not immunogenic in humans.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 87 AA;
XX
Query Match 83.7%; Score 376; DB 17; Length 87;
Best Local Similarity 79.3%; Pred. No. 3.4e-28;
Matches 69; Conservative 11; Mismatches 0; Gaps 0;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFWVRSQSGKLGWIGKATLVDKSTSTAYME 60
Dd 1 QVQLVQSGAEVKKPGASLVSKASGYFTFWVRQAPQRLWGRVITRDTASTAYME 60
QY 61 LSSLRSEDTAVYFCARMGQGTIVTSS 87
Dd 61 LSSLRSEDTAVYFCARMGEGTLVTSS 87
RESULT 4
AAW84097
ID AAW84097 standard; Protein; 117 AA.
XX
AC AAW84097;
XX
DT 15-MAR-1999 (first entry)
XX
DE Humanised anti-alpha-v beta-3 Mab D12H2HC 1-0 VH.
XX
XX Humanised antibody; monoclonal antibody; MAb; antibody engineering;
XX mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
XX cancer; metastasis; rheumatoid arthritis; atherosclerosis;
XX angiogenesis; diabetic retinopathy; inflammation;
XX macular degeneration; osteoporosis; Paget's disease;
XX hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
XX D12H2HC-10.
XX
XX Homo sapiens.
XX
OS Synthetic.
XX

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FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
FT Region 99..106
FT /label= CDR3
XX
XX WO9840488-A1.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US04987.
XX
XX 12-MAR-1997; 97US-0039609.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Johanson KO, Jonak ZL, Taylor AH;
XX
XX WPI; 1999-034590/03.
XX
XX N-PSDB; AAV71799.
XX
XX New anti alpha v beta 3 vitronectin receptor antibodies - used for
XX immunotherapeutic treatment of e.g. diabetic retinopathy,
XX inflammatory disorders, atherosclerosis, restenosis, cancers or
XX osteoporosis
XX
XX Claim 1; Page 58; 97pp; English.
XX
XX This is the amino acid sequence of the heavy chain variable region
XX (VH) of humanised anti-alpha-v beta-3 vitronectin receptor
XX monoclonal antibody D12H2HC 1-0. It is based on the VH sequence
XX (see AAW84095) of human Kabat subgroup I VH, with complementarity
XX determining regions (CDRs) from the murine anti-human alpha-v
XX beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093).
XX 7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)
XX are retained. The humanised heavy chain can be expressed in host
XX cells using nucleic acid molecules (see AAV71799) of the invention.
XX Humanised D12 VL is also provided (see AAW84095). The humanised
XX antibodies can be used for passive immunotherapy of disorders
XX mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
XX angiogenic-related disorders, such as angiogenesis associated
XX with diabetic retinopathy, atherosclerosis and restenosis, chronic
XX inflammatory disorders, macular degeneration, rheumatoid arthritis
XX and cancer, e.g. solid tumour metastasis, and diseases where bone
XX resorption is associated with pathology such as osteoporosis,
XX hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
XX osteolytic lesions produced by bone metastasis, bone loss due to
XX immobilisation or sex hormone deficiency. They can also be used for
XX targeted drug therapy, and for detection and diagnosis.
XX
XX Sequence 117 AA;
XX
Query Match 83.5%; Score 375; DB 20; Length 117;
Best Local Similarity 67.5%; Pred. No. 5.6e-28;
Matches 79; Conservative 6; Mismatches 2; Indels 30; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTFWVRSQSGKLGWIGKATLVDKSTSTAYME 43
Dd 1 QVQLVQSGAEVKKPGASLVSKASGYFTFWVRQAPQRLWGRVITRDTASTAYME 60
QY 44 -----GKATLVDKSTSTAYMELSLRSEDTAVYFCAR-----WGQITVTYSS 87
Dd 61 NQKFKGKATLVDKSTSTAYMELSLRSEDTAVYFCARQNYGSPAYWGQITLVYSS 117
RESULT 5
AAW87965
ID AAW87965 standard; Protein; 135 AA.
XX
XX AAW87965;
XX

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DT 14-NOV-2000 (first entry)
 XX A heavy chain variable region of humanised 351 antibody.
 DE
 XX
 XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
 KW autoimmune disease; infectious disease; inflammatory disorder;
 KW systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
 KW multiple sclerosis; transplant rejection; proliferative disease;
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
 KW aplastic anaemia; myeloid dysplasia syndrome.
 XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX
 XX
 PH Location/Qualifiers
 FT Peptide
 FT 1..19
 FT /note= "signal peptide"
 FT Protein
 FT 20..135
 FT /note= "mature protein"
 FT Region
 FT 50..54
 FT /note= "complementarity determining region 1"
 FT Region
 FT 69..85
 FT /note= "complementarity determining region 2"
 FT Region
 FT 118..124
 FT /note= "complementarity determining region 3"
 FT
 XX WO200047625-A2.
 XX
 XX 17-AUG-2000.
 XX
 XX 09-FEB-2000; 2000WO-US03303.
 XX
 XX 12-FEB-1999; 99US-0249011.
 XX 24-JUN-1999; 99US-0339596.
 XX
 XX (GEMY) GENETICS INST INC.
 XX
 XX Co MS. Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
 XX Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
 XX
 XX WPI; 2000-524532/47.
 XX N-PSDB; AAA59694.
 XX
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived
 XX from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
 XX PT modulates immune responses and can therefore treat e.g. autoimmune
 XX PT diseases, infectious diseases -
 XX
 XX Example 3; Fig 2A; 162pp; English.
 XX
 XX The present sequence represents the heavy chain variable region
 XX of the humanised murine antibody 3D1. The antibody has a binding
 XX specificity to B7 molecules. The antibody is used to construct humanized
 XX immunoglobulins, which comprise an antigen binding region of non-human
 XX origin and a portion of a human immunoglobulin. The humanized
 XX immunoglobulins are useful for treating autoimmune diseases, infectious
 XX diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
 XX mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
 XX inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
 XX also useful for treating a transplant recipient or preventing transplant
 XX rejection in a transplant recipient, and treating proliferative disease
 XX (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
 XX thalassemia and aplastic anaemia), inborn errors of metabolism,
 XX congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 XX
 XX Sequence 135 AA;
 SQ
 Query Match 82.5%; Score 370.5; DB 21; Length 135;
 Best Local Similarity 66.4%; Pred. No. 1.7e-27;
 Matches 77; Conservative 8; Mismatches 2; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYST-----WVROSPGKLEWI----- 43
 DB 20 QVQLVQSGAEVKKPGSSVKVCKASGYTFDTYAIQWVROAPGQGLEWIGVINYDNTNY 79
 QY 44 -----GKATLTVDKSTSTAYWELSSLRSEDTAVYFCAR-----WGQGTIVTVSS 87
 DB 80 NQRFKGRATVTDKSTSTAYWELSSLRSEDTAVYCARAAWYNDYWGQGTIVTVSS 135
 RESULT 6
 ID AAW06442 standard; Protein; 136 AA.
 XX
 AC AAW06442;
 XX
 DT 04-FEB-1997 (first entry)
 XX
 DE HuMc3 VH region.
 XX
 KW Humanised antibody; variable heavy region; buried residue modification;
 KW VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMF; lactation;
 KW fat globule membrane; murine; mammary; epithelial cell; breast cancer;
 KW breast membrane glycoprotein; therapy; immunotherapy.
 XX
 OS Synthetic.
 XX WO9608565-A2.
 XX
 XX 21-MAR-1996.
 XX
 XX 14-SEP-1995; 95WO-US11683.
 XX
 XX 07-JUN-1995; 95US-0487598.
 XX 16-SEP-1994; 94US-0307868.
 XX
 XX (CANC-) CANCER RES FUND CONTRA COSTA.
 XX
 XX Ceriani RI, Do Couto FJR, Peterson JA;
 XX WPI; 1996-179941/18.
 XX N-PSDB; AAT42717.
 XX
 XX Recombinant Mc3 antibody which binds BA46 antigen of HMF -
 XX PT comprises a modified heavy or light chain variable region, useful in
 XX PT the diagnosis and therapy of breast cancer
 XX
 XX Claim 13; Fig 18; 91pp; English.
 XX
 XX This sequence represents the variable heavy (VH) chain of the humanised
 XX murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the
 XX buried residue modification technique, where important non-human
 XX framework residues are unaffected. The Mc3 antibody binds to the BA46
 XX antigen of the human milk fat globule (HMF). The milk fat globule
 XX membrane is derived from the apical surface of the mammalian epithelial
 XX cell during lactation, and therefore is a source for breast membrane
 XX glycoproteins. The antibody can be used in an in vitro method to detect
 XX a HMF antigen (or antigen fragment), and to diagnose the presence of the
 XX antigen in a subject. The antibody can also be used to deliver an agent
 XX to a target (within a subjects body), containing a HMF antigen. The
 XX antibodies can also be used for diagnosis, prognosis, and therapeutic
 XX applications of breast cancer. As the humanised antibodies retain their
 XX high affinity binding to the antigen, they are useful for
 XX immunodiagnostic and immunotherapeutic applications in humans.
 XX
 XX Sequence 136 AA;
 SQ
 Query Match 82.4%; Score 370; DB 17; Length 136;
 Best Local Similarity 67.5%; Pred. No. 1.9e-27;
 Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;
 QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYST-----WVROSPGKLEWIG----- 44
 DB 20 EVQLVQSGAEVKKPGASVKVCKASGYSTGYTMHWVKQSPGMNLEWIGLINPYNGTIV 79

QY 45 -----KATLVKSTSTAYMELSSLRSEDYAVFCAR-----WGQTTVTYSS 87
 DB 80 NQKFDKATLVKSTSTAYMELSSLRSEDYAVFCARWRYTMDYWGQTTVTYSS 136

RESULT 7
 AAB12168
 ID AAB12168 standard; Protein; 115 AA.
 XX
 AC AAB12168;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.
 XX
 KW Humanised antibody; HBV surface antigen pre-S1; mouse;
 KW human; hepatitis B; liver cirrhosis; liver cancer.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX
 PN WO200031141-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 19-NOV-1999; 99WO-KR00699.
 XX
 PR 19-NOV-1998; 98KR-0049663.
 XX
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
 PA (GREC) KOREA GREEN CROSS CORP.
 XX
 PI Hong HJ, Ryu CJ, Hur H;
 XX
 DR WPI; 2000-400049/34.
 DR N-PSDB; AAA62118.
 XX
 XX Humanized antibody specific for hepatitis B virus surface antigen
 PT pre-S1, containing humanized heavy and light chain regions, useful for
 PT preventing hepatitis B virus (HBV) infection and for treating chronic
 PT hepatitis B -
 XX
 PS Claim 2; Fig 1; 61pp; English.

CC Hepatitis B virus (HBV) is responsible for hepatitis infection in
 CC humans, which may progress to liver cirrhosis or cancer. One of HBV's
 CC surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1
 CC antigen may efficiently neutralise HBV. The present invention relates to
 CC humanised antibodies specific for HBV surface antigen pre-S1. The
 CC humanised antibodies are useful for preventing HBV infection and for
 CC treating chronic hepatitis B. The Complementarity Determining Regions of
 CC mouse pre-S1 antibody KR127 were grafted onto human antibody to produce
 CC the humanised antibodies of the present invention. The present sequence
 CC is the humanised pre-S1 antibody HKR127HC(I) heavy chain variable region
 CC (VH). The coding sequence for the present sequence was produced from the
 CC coding sequence of the mouse pre-S1 antibody VH sequence (AAA62115).
 XX
 SQ Sequence 115 AA;

Query Match 81.1%; Score 364; DB 21; Length 115;
 Best Local Similarity 67.0%; Pred. No. 6e-27;
 Matches 77; Conservative 6; Mismatches 4; Indels 28; Gaps 3;

QY 1 QIQLVSGGVKKPGASVRSCKAGYSFT-----WVRSPPGKLEWT-----43
 DB 1 QIQLVSGAEVKKPGASVRSCKAGYAFSSWNVRQAPGQGLEWIGRIYPGDGTNY 60

QY 44 -----GRATLVKSTSTAYMELSSLRSEDYAVFCAR-----WGQTTVTYSS 87
 DB 61 AQKFGKATLVKSTSTAYMELSSLRSEDYAVFCAREYDEAYWGQTTVTYSS 115

RESULT 8

AAW90935
 ID AAW90935 standard; Protein; 470 AA.
 XX
 AC AAW90935;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed heavy chain Heu 3 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI; 2000-258930/23.
 DR N-PSDB; AA11646.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PS Claim 2; Page 180-182; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.

XX SQ Sequence 470 AA;
Query Match 81.1%; Score 364; DB 21; Length 470;
Best Local Similarity 63.6%; Pred. No. 2.3e-26;
Matches 77; Conservative 7; Mismatches 3; Indels 34; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRYSCASGYFTFTSYMWQVRQAPGGLEWMEIDPSDSYTN 43
DB 20 QVQLVQSGAEVKKFGASVKYSCASGYFTFTSYMWQVRQAPGGLEWMEIDPSDSYTN 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGITTVTVS 86
DB 80 NQKFKGKATLTVDSTSTAYMELSLRSEDATVYICARNRDSNNWYFDWVGQGLTVTVS 139
QY 87 S 87
DB 140 S 140
RESULT 9
ABBY4904
ID ABBY4904 standard; Protein; 470 AA.
XX ABBY4904;
AC ABBY4904;
XX 26-APR-2002 (first entry)
DT Mouse humanised anti-Fas antibody related protein SRQ ID NO 9.
DE Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW autoimmune disease; allergy; atopic.
XX Mus musculus.
OS
XX JP2001342148-A.
XX 11-DEC-2001.
XX 28-MAR-2001; 2001JP-0093106.
XX 29-MAR-2000; 2000JP-0090918.
XX (SANY) SANKYO CO LTD.
XX WPI; 2002-145113/19.
XX N-PSDB; ABL45926.
XX Drug containing humanised anti-Fas antibody, used for preventing and
XX treating autoimmune diseases, allergy, and atopy -
XX Example 4 (Preparatory); Page 79-80; 194pp; Japanese.
XX The invention relates to a preventive or treating agent for diseases
XX caused by abnormality in Fas/Fas ligand system containing as the active
XX component an antibody having as the light chain subunit a polypeptide
XX containing residues 1-218 of one of 3, 239 residue amino acid sequences,
XX or residues 1-451 of one of 3, 470 residue amino acid sequences, all
XX fully defined in the specification and having an activity of combining
XX specifically with mammalian Fas and an activity of inducing apoptosis
XX in a cell expressing Fas. The agent has immunosuppressive and
XX antiallergic activity and is used for preventing and treating autoimmune
XX diseases, allergy, atopy and others.
XX SQ Sequence 470 AA;
Query Match 81.1%; Score 364; DB 23; Length 470;
Best Local Similarity 63.6%; Pred. No. 2.3e-26;
Matches 77; Conservative 7; Mismatches 3; Indels 34; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRYSCASGYFTFTSYMWQVRQAPGGLEWMEIDPSDSYTN 43

DB 20 QVQLVQSGAEVKKPGASVKYSCASGYFTFTSYMWQVRQAPGGLEWMEIDPSDSYTN 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQGITTVTVS 86
DB 80 NQKFKGKATLTVDSTSTAYMELSLRSEDATVYICARNRDSNNWYFDWVGQGLTVTVS 139
QY 87 S 87
DB 140 S 140
RESULT 10
AAR92218
ID AAR92218 standard; Protein; 116 AA.
XX AAR92218;
AC AAR92218;
XX 28-MAY-1996 (first entry)
DT Humanised LL2 MAb VH region.
DE Humanised antibody; monoclonal antibody; MAb; LL2; B-cell lymphoma;
KW leukaemia; therapy; diagnosis; complementarity determining region;
KW CDR; antibody engineering.
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
FT Region 99..105
FT /label= CDR3
XX WO9604925-A1.
XX 22-FEB-1996.
XX 11-AUG-1995; 95WO-US09641.
XX 12-AUG-1994; 94US-0289576.
XX (IMMU-) IMMUNOMEDICS INC.
XX Hansen H, Leung S;
XX WPI; 1996-139454/14.
XX N-PSDB; AAT15804.
XX Chimeric and humanised LL2 antibodies - used to produce conjugates
XX for the therapy and diagnosis of B-cell lymphoma(s) and
XX leukaemia(s).
XX Claim 5; Page 39; 70pp; English.
XX The complementarity determining regions (CDRs) of mouse monoclonal
XX antibody (MAb) LL2 VK (AAR92215) and VH (AAR92216) regions were
XX recombinantly linked to the framework sequences of human VK and VH
XX regions, respectively, to give humanised LL2 VK (AAR92217) and VH
XX (AAR92218). These were subsequently linked, respectively, to human
XX kappa and IgG1 constant regions. A humanised MAb was obt'd. that
XX retained the B-lymphoma and leukaemia cell targeting and
XX internalisation characteristics of the parental LL2 MAb, and which
XX exhibited a lowered HAMA reaction. It can be linked to e.g. a
XX cytostatic agent for therapeutic appln.
XX SQ Sequence 116 AA;
Query Match 81.0%; Score 363.5; DB 17; Length 116;
Best Local Similarity 64.7%; Pred. No. 6.7e-27;
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVVRVSKASGYST-----WVRQSPKGLWIG----- 44
 Db 1 QVOLVQSGAEVKKPGSSVKVSKASGYFTTYSWLHWVRQAPQGLWIGYINPRNDYTEY 60
 QY 45 -----KATLTVDKSTSTAYMELSSLRSDTAVYFCAR-----WGQTTVTVSS 87
 Db 61 NONFKDKATITADESTNTAYMELSSLRSDTAFYFCARRDITTFYWGQTTVTVSS 116

RESULT 11
 AAW27698
 ID AAW27698 standard; Protein; 116 AA.
 XX
 AC AAW27698;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Variable heavy chain of MAb hLL2.
 XX
 KW Variable heavy chain; B cell; monoclonal antibody; MAb; hLL2;
 KW B cell lymphoma; lymphocytic leukaemia cell; murine; humanised;
 KW diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma;
 KW chronic lymphocytic leukaemia.
 XX
 OS Chimeric - Mus sp.
 XX Chimeric - Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /note= "complementarity determining region 1"
 FT Region 50..66
 FT /note= "complementarity determining region 2"
 FT Region 99..105
 FT /note= "complementarity determining region 3"
 FT
 XX WO9734632-A1.
 PN
 XX
 XX 25-SEP-1997.
 PD
 PF 19-MAR-1997; 97WO-US04196.
 XX
 PR 20-MAR-1996; 96US-0013709.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S, Qu Z;
 XX
 DR WPI; 1997-479995/44.
 DR N-PSDB; AAT88131.
 XX
 PT Monoclonal antibody engineered to contain glycosylation site - in
 PT non-Fc constant heavy or light chain region, useful to diagnose or
 PT treat B cell malignancies, e.g. non-Hodgkins lymphoma
 XX
 PS Example 3; Fig 5B; 88pp; English.
 XX
 CC The present sequence is the variable heavy chain of the
 CC B cell specific monoclonal antibody (MAb) hLL2. hLL2 is a highly
 CC specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell
 CC humanised murine MAb. The MAb can be used to diagnose or treat B
 CC cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 CC lymphocytic leukaemia.
 XX
 SQ Sequence 116 AA;
 Query Match 81.0%; Score 363.5; DB 18; Length 116;
 Best Local Similarity 64.7%; Pred. No. 6.7e-27;
 Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVVRVSKASGYST-----WVRQSPKGLWIG----- 44
 Db 1 QVOLVQSGAEVKKPGSSVKVSKASGYFTTYSWLHWVRQAPQGLWIGYINPRNDYTEY 60

QY 45 -----KATLTVDKSTSTAYMELSSLRSDTAVYFCAR-----WGQTTVTVSS 87
 Db 61 NONFKDKATITADESTNTAYMELSSLRSDTAFYFCARRDITTFYWGQTTVTVSS 116

RESULT 12
 AAR29017
 ID AAR29017 standard; Protein; 135 AA.
 XX
 AC AAR29017;
 XX
 DT 25-MAR-2003 (updated)
 DT 30-MAR-1993 (first entry)
 XX
 DE pUC-RVh-1220d.
 XX
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
 KW complementarity determining region; monoclonal; hybridoma; PCR;
 KW plasmid; polymerase chain reaction; amplify.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Leader peptide"
 FT Region 20..49
 FT /label= PR1
 FT Region 50..54
 FT /label= CDR1
 FT Region 55..68
 FT /label= PR2
 FT Region 69..85
 FT /label= CDR2
 FT Region 86..117
 FT /label= PR3
 FT Region 118..124
 FT /label= CDR3
 FT Region 125..135
 FT /label= PR4
 XX
 PN WO9219759-A1.
 XX
 PD 12-NOV-1992.
 XX
 PF 24-APR-1992; 92WO-JP00544.
 XX
 PR 25-APR-1991; 91JP-0095476.
 PR 19-FEB-1992; 92JP-0032084.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 XX WPI; 1992-398882/48.
 DR N-PSDB; AAQ31391.
 DR
 XX Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 XX
 PS Disclosure; Page 159-60; 207pp; Japanese.
 XX
 CC The sequences given in AAR29016-17 are portions of monoclonal antibodies
 CC which were encoded by plasmids contained within the mouse hybridoma,
 CC AUK12-20. The DNA encoding the complementarity determining regions
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells
 CC were transformed with plasmids containing fragments of the antibody
 CC gene which caused the production of the antibody from the hybridoma
 CC cell line.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 135 AA;

Query Match 81.0%; Score 363.5; DB 13; Length 135;
 Best Local Similarity 65.5%; Pred. No. 7.8e-27;
 Matches 76; Conservative 7; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRQSPGKGLWMI----- 43
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTFYWMQWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87
 DB 80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYFCARGLRGGYFDYWGQGTITVSS 139

RESULT 13
 AAW65773
 ID AAW65773 standard; Protein; 139 AA.
 XX AC AAW65773;
 XX DT 16-NOV-1998 (first entry)
 XX DE Anti-human HM1.24 antibody heavy chain variable region r.
 XX KW Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;
 XX KW pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 XX OS Synthetic.
 XX FH Key
 XX FT Peptide
 XX FT Peptide
 XX FT Peptide
 XX FT Peptide
 XX PN WO9835698-A1.
 XX PD 20-AUG-1998.
 XX PF 12-FEB-1998; 98WO-JP00568.
 XX PR 12-FEB-1997; 97JP-0041410.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Koishihara Y, Yoshimura Y;
 XX WPI; 1998-456869/39.
 XX DR N-PSDB; AAV07581.
 XX Treatment of lymphocytic tumours using cytotoxic antibody - binding
 PT to specific antigen such as HM1.24 and effective against T-cell
 PT tumours and B-cell tumours other than myeloma
 XX Disclosure; Page 47-48; 82pp; Japanese.
 CC The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be
 CC used in the treatment of lymphocytic tumours, including T-cell tumours
 CC and B-cell tumours other than myeloma. The antibody is preferably
 CC monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or
 CC humanised, and preferably contains a human antibody constant region C
 CC gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an
 CC anti-human HM1.24 antibody or an antibody which binds to an epitope
 CC recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful
 CC in the treatment of lymphocytic tumours such as acute or chronic B
 CC lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or
 CC chronic T lymphocytic leukaemia.
 XX SQ Sequence 139 AA;

Query Match 81.0%; Score 363.5; DB 19; Length 139;
 Best Local Similarity 62.5%; Pred. No. 8e-27;
 Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRQSPGKGLWMI----- 43
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTFYWMQWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRQSPGKGLWMI----- 43
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTFYWMQWVRQAPGQGLEWMGSIFFPGDTRY 79

QY 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87
 DB 80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYFCARGLRGGYFDYWGQGTITVSS 139

RESULT 14
 AAW65774
 ID AAW65774 standard; Protein; 139 AA.
 XX AC AAW65774;
 XX DT 16-NOV-1998 (first entry)
 XX DE Anti-human HM1.24 antibody heavy chain variable region s.
 XX KW Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours;
 XX KW pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 XX OS Synthetic.
 XX FH Key
 XX FT Peptide
 XX FT Peptide
 XX FT Peptide
 XX FT Peptide
 XX PN WO9835698-A1.
 XX PD 20-AUG-1998.
 XX PF 12-FEB-1998; 98WO-JP00568.
 XX PR 12-FEB-1997; 97JP-0041410.
 XX PA (CHUS) CHUGAI SEIYAKU KK.
 XX PI Koishihara Y, Yoshimura Y;
 XX WPI; 1998-456869/39.
 XX DR N-PSDB; AAV07582.
 XX Treatment of lymphocytic tumours using cytotoxic antibody - binding
 PT to specific antigen such as HM1.24 and effective against T-cell
 PT tumours and B-cell tumours other than myeloma
 XX Disclosure; Page 48-49; 82pp; Japanese.
 CC The anti-human HM1.24 antibody is the preferred cytotoxic antibody to be
 CC used in the treatment of lymphocytic tumours, including T-cell tumours
 CC and B-cell tumours other than myeloma. The antibody is preferably
 CC monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or
 CC humanised, and preferably contains a human antibody constant region C
 CC gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an
 CC anti-human HM1.24 antibody or an antibody which binds to an epitope
 CC recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful
 CC in the treatment of lymphocytic tumours such as acute or chronic B
 CC lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or
 CC chronic T lymphocytic leukaemia.
 XX SQ Sequence 139 AA;

Query Match 81.0%; Score 363.5; DB 19; Length 139;
 Best Local Similarity 62.5%; Pred. No. 8e-27;
 Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSTFT-----WVRQSPGKGLWMI----- 43
 DB 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTFYWMQWVRQAPGQGLEWMGSIFFPGDTRY 79

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Job time : 20.2873 secs

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Db 80 SQKFKGRVTITADKSTAYMELSLRSEDYAVYFCARGLRGGYFDYWGQGGTTVTVSS 139

RESULT 15
AAW62205
ID AAW62205 standard; Protein; 139 AA.
XX
AC AAW62205;
XX
DT 21-SEP-1998 (first entry)
XX
DE Humanised anti-HM1.24 antibody H chain V region HEF-RVHR-AHM g-gamma-1.
XX
KW Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR; CDR;
KW framework region; complementarity determining region; antigenicity.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
FN WO9814580-A1.
XX
PD 09-APR-1998.
XX
PF 03-OCT-1997; 97WO-JP03353.
XX
PR 04-OCT-1996; 96JP-0264756.
XX
PA (CHUS ) CHUGAI SEIYAKU KK.
XX
PI Koishihara Y, Kosaka M, Ohtomo T, Ono K, Teuchiya M;
PI Yoshimura Y;
XX
DR WPI; 1998-286421/25.
DR N-PSDB; AAV33357.
XX
PT Humanised anti-HM1.24 antibody - for treatment of myeloma
XX
PS Claim 68; Page 127-128; 210pp; Japanese.
XX
CC A humanised anti-HM1.24 antibody has been developed which comprises
CC human L and H chain C regions, and L and/or H chain V regions
CC containing material originating in mouse anti-HM1.24 antibody. The V
CC regions contain framework (FR) regions of human origin and
CC complementarity determining regions (CDR) of mouse origin, leading to
CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and
CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the
CC L chain V region are derived from human subtype HSG1 (e.g. from human
CC antibody RE1) and the FR regions of the H chain V region are derived
CC from human subtype HSG1 (e.g. FR1-3 from human antibody HG3 and FR4
CC from human antibody JH6). The present sequence represents an H chain
CC V region from the present invention. The antibodies are used for
CC the treatment of myeloma, especially by injection, intravenously,
CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
CC (especially 5-100) mg/kg body weight. The humanised antibody has low
CC antigenicity and is therefore effective therapeutically in humans.
XX
SQ Sequence 139 AA;

Query Match 81.0%; Score 363.5; DB 19; Length 139;
Best Local Similarity 62.5%; Pred. NO. 8e-27;
Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKPGASVRSVCKASGYSFT-----WVRQSPGKGLEWI----- 43
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Db 20 QVQLVQSGGEVKPGASVRSVCKASGYTFTPYMWQVWVQAPQGLEWMGSIFFPGDGT 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 -----GKATLTVDKSTAYMELSLRSEDYAVYFCAR-----WQGGTTVTVSS 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 SQKFKGRVTMTADKSTAYMELSLRSEDYAVYFCARGLRGGYFDYWGQGGTTVTVSS 139
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 13.9048 Seconds
(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pdb.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pdb.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pdb.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pdb.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pdb.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pdb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	100.0	87	11	US-09-990-586-91
2	449	100.0	87	11	US-09-990-586-92
3	449	100.0	87	12	US-10-230-880-91
4	449	100.0	87	12	US-10-230-880-92
5	441	98.2	87	12	US-09-990-586-93
6	441	98.2	87	12	US-10-230-880-93
7	439	97.8	87	11	US-09-990-586-90
8	439	97.8	87	12	US-10-230-880-90
9	438	97.6	87	11	US-09-990-586-94
10	438	97.6	87	12	US-10-230-880-94
11	434	96.7	87	11	US-09-990-586-96
12	434	96.7	87	12	US-10-230-880-96
13	431	96.0	87	11	US-09-990-586-95
14	431	96.0	87	12	US-10-230-880-95
15	430	95.8	87	11	US-09-990-586-89

Sequence 89, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 166, Appl
Sequence 172, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 168, Appl
Sequence 86, Appl
Sequence 200, Appl
Sequence 7, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 159, Appl
Sequence 167, Appl
Sequence 167, Appl
Sequence 5, Appl
Sequence 157, Appl
Sequence 171, Appl
Sequence 6, Appl
Sequence 24, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 78, Appl
Sequence 63, Appl
Sequence 199, Appl
Sequence 83, Appl
Sequence 83, Appl
Sequence 147, Appl

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ALIGNMENTS

RESULT 1
US-09-990-586-91
; Sequence 91, Application US/09990586
; Publication No. US2003010960A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-91

Query Match 100.0%; Score 449; DB 11; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QIQLVQSGGVKPKGASVRVSCASGYSTWVQSPKGLWIGKATLTVDKSTSTAYME 60
Db 1 QIQLVQSGGVKPKGASVRVSCASGYSTWVQSPKGLWIGKATLTVDKSTSTAYME 60

Qy 61 LSSLRSEDTAVYFCARWGQGTIVTSS 87
Db 61 LSSLRSEDTAVYFCARWGQGTIVTSS 87

RESULT 2
US-09-990-586-92
; Sequence 92, Application US/09990586

US-10-230-880-93
; Sequence 93, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-93

Query Match 98.2%; Score 441; DB 12; Length 87;
Best Local Similarity 98.9%; Pred. No. 5.7e-37;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 QIQLVQSGPEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSDETAVFPCARWGQTTVTSS 87
DB 61 LSSLRSDETAVFPCARWGQTTVTSS 87

RESULT 7
US-09-990-586-90
; Sequence 90, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-90

Query Match 97.8%; Score 439; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 9.1e-37;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 1 QIQLVQSGGELVKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSDETAVFPCARWGQTTVTSS 87
DB 61 LSSLRSDETAVFPCARWGQTTVTSS 87

RESULT 8
US-10-230-880-90
; Sequence 90, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-90

Query Match 97.8%; Score 439; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 9.1e-37;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGGELVKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSDETAVFPCARWGQTTVTSS 87
DB 61 LSSLRSDETAVFPCARWGQTTVTSS 87

RESULT 9
US-09-990-586-94
; Sequence 94, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-94

Query Match 97.8%; Score 438; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 1.1e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGPELKKPGASVRVSKASGYSTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSDETAVFPCARWGQTTVTSS 87
DB 61 LSSLRSDETAVFPCARWGQTTVTSS 87

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RESULT 10
US-10-230-880-94
; Sequence 94, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-94

Query Match          97.6%; Score 438; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 1.1e-36;
Matches 85; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 11
US-09-990-586-96
; Sequence 96, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-96

Query Match          96.7%; Score 434; DB 11; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.9e-36;
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
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RESULT 12
US-10-230-880-96
; Sequence 96, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-96

Query Match          96.7%; Score 434; DB 12; Length 87;
Best Local Similarity 97.7%; Pred. No. 2.9e-36;
Matches 85; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
DB 61 LSSLRSEDTAVYFCARWGQGTITVSS 87

RESULT 13
US-09-990-586-95
; Sequence 95, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-95

Query Match          96.0%; Score 431; DB 11; Length 87;
Best Local Similarity 96.6%; Pred. No. 5.7e-36;
Matches 84; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPKGLGWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDTAVYFCARWGQGTITVSS 87
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Db 61 LSSLRSEDVAVFCARWGQTTVTSS 87

Search completed: January 13, 2004, 13:13:43
Job time : 13.9048 secs

Db 61 LSSLRSEDVAVFCARWGQTTVTSS 87

RESULT 14

US-10-230-880-95
; Sequence 95, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-95

Query Match 96.0%; Score 431; DB 12; Length 87;
Best Local Similarity 96.6%; Pred. No. 5.7e-36;
Matches 84; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGVKPGASVRVSKASGYFTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QIQLVSGPELVKPGASVRVSKASGYFTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDVAVFCARWGQTTVTSS 87
DB 61 LSSLRSEDVAVFCARWGQTTVTSS 87

RESULT 15

US-09-990-586-89
; Sequence 89, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-89

Query Match 95.8%; Score 430; DB 11; Length 87;
Best Local Similarity 95.4%; Pred. No. 7.2e-36;
Matches 83; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QIQLVSGGVKPGASVRVSKASGYFTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60
DB 1 QMQLQSGGELVKPGASVRVSKASGYFTWVRQSPGKLEWIGKATLTVDKSTSTAYME 60

QY 61 LSSLRSEDVAVFCARWGQTTVTSS 87

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 7.52227 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-91

Perfect score: 449

Sequence: 1 QIQLVSGGVKPKGASVRV.....DTAVYFCARWGQTTVTVSS 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 4231058 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	86.0	87	1	US-08-497-312-16
2	370	82.4	117	4	US-08-525-539A-78
3	370	82.4	136	4	US-08-525-539A-63
4	364.5	81.2	86	1	US-08-497-312-27
5	363.5	81.0	116	1	US-08-690-102A-8
6	363.5	81.0	116	3	US-09-137-902-8
7	363.5	81.0	116	3	US-09-155-107-8
8	363.5	81.0	116	5	PCT-US95-09641-8
9	363.5	81.0	135	1	US-08-137-117D-102
10	363.5	81.0	135	2	US-08-436-717-102
11	363.5	81.0	139	4	US-09-355-925-7
12	363.5	81.0	139	4	US-09-355-925-8
13	362.5	80.7	116	2	US-08-561-521-41
14	362.5	80.7	116	5	PCT-US95-01219-41
15	360	80.2	119	1	US-08-498-516-10
16	360	80.2	136	4	US-09-450-520A-8
17	360	80.2	222	1	US-08-458-516-22
18	360	80.2	235	1	US-08-458-516-23
19	360	80.2	449	1	US-08-458-516-13
20	359.5	80.1	116	1	US-07-634-278-5
21	359.5	80.1	116	1	US-07-634-278-57
22	359.5	80.1	116	1	US-07-634-278-73
23	359.5	80.1	116	1	US-08-477-728-5
24	359.5	80.1	116	1	US-08-477-728-57
25	359.5	80.1	116	1	US-08-477-728-73
26	359.5	80.1	116	1	US-08-474-040-5
27	359.5	80.1	116	1	US-08-474-040-57

28	359.5	80.1	116	1	US-08-474-040-73	Sequence 73, Appl
29	359.5	80.1	116	1	US-08-487-200-5	Sequence 5, Appl
30	359.5	80.1	116	1	US-08-487-200-57	Sequence 57, Appl
31	359.5	80.1	116	1	US-08-487-200-73	Sequence 73, Appl
32	359.5	80.1	116	1	US-08-488-113B-169	Sequence 169, App
33	359.5	80.1	116	1	US-08-477-484B-169	Sequence 169, App
34	359.5	80.1	116	1	US-08-107-669D-55	Sequence 55, Appl
35	359.5	80.1	116	1	US-08-472-788A-86	Sequence 86, Appl
36	359.5	80.1	116	2	US-08-477-531B-55	Sequence 55, Appl
37	359.5	80.1	116	2	US-08-646-360-169	Sequence 169, App
38	359.5	80.1	116	2	US-08-842A-86	Sequence 86, Appl
39	359.5	80.1	116	3	US-08-934-841-1	Sequence 1, Appl
40	359.5	80.1	116	3	US-09-393-409-1	Sequence 1, Appl
41	359.5	80.1	116	3	US-08-839-785-169	Sequence 169, App
42	359.5	80.1	116	3	US-09-136-389-169	Sequence 169, App
43	359.5	80.1	116	3	US-08-484-537-5	Sequence 5, Appl
44	359.5	80.1	116	3	US-08-484-537-57	Sequence 57, Appl
45	359.5	80.1	116	3	US-08-484-537-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-08-497-312-16

; Sequence 16, Application US/08497312

; Patent No. 5712120

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Method for obtaining modified

; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR

; STREET: 215 Y 15, ATABEY PLAYA

; CITY: HAVANA

; STATE:

; COUNTRY: CUBA

; ZIP: 11600

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/497,312

; FILING DATE: 30-JUN-1995

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: CU 80/94

; FILING DATE: 30-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BOND, LAURENCE B.

; REGISTRATION NUMBER: 30,549

; REFERENCE/DOCKET NUMBER: 2629US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 801/532-1922

; TELEFAX: 801/531-9168

; TELEX: 388961 1PM04UT

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 87 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-08-497-312-16

Query Match 86.0%; Score 386; DB 1; Length 87;

Best Local Similarity 81.6%; Pred. No. 2.6e-33;

Matches 71; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
Db 1 QVQLVQSGAEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87
Db 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87

RESULT 2
US-08-525-539A-78
; Sequence 78, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-63

Query Match 82.4%; Score 370; DB 4; Length 136;
Best Local Similarity 67.5%; Pred. No. 2e-31;
Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
Db 20 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTHWVKQSPGMNLEWIGLINPYNGTIVY 79
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87
Db 80 NQKFDKATLTVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTITVSS 136

RESULT 4
US-08-497-312-27
; Sequence 27, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
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QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
Db 1 QVQLVQSGAEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
QY 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87
Db 61 LSSLRSSEDTAVYFCARWGQGTITVSS 87

RESULT 2
US-08-525-539A-78
; Sequence 78, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-525-539A-78

Query Match 82.4%; Score 370; DB 4; Length 117;
Best Local Similarity 67.5%; Pred. No. 1.7e-31;
Matches 79; Conservative 4; Mismatches 4; Indels 30; Gaps 3;

QY 1 QIQLVQSGGEVKPGASVRSCKASGYSTFWRSQPGKLEWIGKATLTVDKSTSTAYME 60
Db 1 EVQLVQSGAEVKPGASVRSCKASGYSTFGYTHWVKQSPGMNLEWIGLINPYNGTIVY 60
QY 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTITVSS 87
Db 61 NQKFDKATLTVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTITVSS 117

RESULT 3
US-08-525-539A-63
; Sequence 63, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
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APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 LPMO4UT
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-27

Query Match 81.2%; Score 364.5; DB 1; Length 86;
Best Local Similarity 79.3%; Pred. No. 4,4e-31;
Matches 69; Conservative 10; Mismatches 7; Indels 1; Gaps 1;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
DB 1 QVOLVQSGAEVKKPGASLKVSKASGY-FTWVRQAPQGRLEWVGRTITRDTASTAYME 59
QY 61 LSSLRSEDATVYFCARWGGTTVTSS 87
DB 60 LSSLRSEDATVYFCARWGGTTVTSS 86

RESULT 5

US-08-690-102A-8
Sequence 8, Application US/08690102A
Patent No. 5789554
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 9041136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-902-8

SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-690-102A-8

Query Match 81.0%; Score 363.5; DB 1; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYFTWVRQSPGKGLWIGKATLTVDKSTSTAYME 60
DB 1 QVOLVQSGAEVKKPGASVRVSKASGYFTTSTLHWVRQAPQCGLEWIGYINPRNDYTEY 60
QY 45 -----KATLTVDKSTSTAYMELSLRSEDATVYFCAR-----WGQFTTIVTSS 87
DB 61 NQNFKDKAITADESINTAYMELSLRSEDATVYFCARRDITTFYWGQFTTIVTSS 116

RESULT 6

US-09-127-902-8
Sequence 8, Application US/09127902
Patent No. 6187287
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 9041136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-127-902-8

Query Match 81.0%; Score 363.5; DB 3; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRVSKASGYFTTSTLHWVRQAPQCGLEWIGKATLTVDKSTSTAYME 60
DB 1 QVOLVQSGAEVKKPGASVRVSKASGYFTTSTLHWVRQAPQCGLEWIGYINPRNDYTEY 60

QY 45 -----KATLVDSKSTAYMELSSLRSDTAVYFCAR-----WGQGTITVTVSS 87
DB 61 NQNFKQKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTITVTVSS 116

RESULT 7

US-09-155-107-8

; Sequence 8, Application US/09155107

; Patent No. 6254868

; GENERAL INFORMATION:

; APPLICANT: LEUNG, Shui-on

; APPLICANT: HANSEN, Hans

; APPLICANT: QU, Zhengxing

; TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES

; FILE REFERENCE: 018733/0879

; CURRENT APPLICATION NUMBER: US/09/155,107

; CURRENT FILING DATE: 1998-11-17

; EARLIER APPLICATION NUMBER: WO PCT/US97/04196

; EARLIER FILING DATE: 1997-03-19

; EARLIER APPLICATION NUMBER: US 60/013,703

; EARLIER FILING DATE: 1996-03-20

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 8

; LENGTH: 116

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-155-107-8

Query Match 81.0%; Score 363.5; DB 3; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRYVSKASGYSTFT-----WVRSQPGKGLWIG-----44
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYLHWVRQAPGGQLEWIGVINPRNDYTEY 60

QY 45 -----KATLVDSKSTAYMELSSLRSDTAVYFCAR-----WGQGTITVTVSS 87

DB 61 NQNFKQKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTITVTVSS 116

RESULT 8

PCT-US95-09641-8

; Sequence 8, Application PC/TUS9509641

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED

; ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS

; NUMBER OF SEQUENCES: 21

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/09641

; FILING DATE: 11-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/289,576

; FILING DATE: 12-AUG-1994

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 116 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-09641-8

Query Match 81.0%; Score 363.5; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRYVSKASGYSTFT-----WVRSQPGKGLWIG-----44
DB 1 QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYLHWVRQAPGGQLEWIGVINPRNDYTEY 60

QY 45 -----KATLVDSKSTAYMELSSLRSDTAVYFCAR-----WGQGTITVTVSS 87

DB 61 NQNFKQKATITADESTNTAYMELSSLRSDTAVYFCARRDITTFYWGQGTITVTVSS 116

RESULT 9

US-08-137-117D-102

; Sequence 102, Application US/08137117D

; Patent No. 5795965

; GENERAL INFORMATION:

; APPLICANT: TSUCHIYA, Masayuki

; APPLICANT: SATO, Koh

; APPLICANT: BENDIG, Mary

; APPLICANT: JONES, Steven

; APPLICANT: SALDANHA, Jose

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; INTERLEUKIN-6 RECEPTOR

; NUMBER OF SEQUENCES: 158

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/137,117D

; FILING DATE: 20-DEC-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JPS92/00544

; FILING DATE: 24-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 4-32084

; FILING DATE: 19-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 3-95476

; FILING DATE: 25-APR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 53466/136/AAOK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 102:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 135 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-137-117D-102

Query Match 81.0%; Score 363.5; DB 1; Length 135;
Best Local Similarity 65.5%; Pred. No. 9.2e-31;
Matches 76; Conservative 7; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRYVSKASGYSTFT-----WVRSQPGKGLWIG-----43
DB 20 QVQLVQSGAEVKKPGSSVKVSKASGYSTFTSYLHWVRQAPGGQLEWIGVINPRNDYTEY 79

QY 44 -----GKATLVDSKSTAYMELSSLRSDTAVYFCAR-----WGQGTITVTVSS 87

Db 80 NQKFGKVTMTVDTSTNTAYMELSLRSEDYAVVYCARGNRFAYWGQGLTVTVSS 135

RESULT 10

US-08-436-717-102
; Sequence 102, Application US/08436717
; Patent No. 581790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-102

Query Match 81.0%; Score 363.5; DB 2; Length 135;
Best Local Similarity 65.5%; Pred. No. 9.2e-31;
Matches 76; Conservative 7; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW-----43

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYSTSYIHVWRQAPGQGLEWIGYIDPENGQTSY 79

QY 44 -----GKATLVDKSTSTAYMELSLRSEDYAVFCAR-----WGQGTIVTVSS 87

Db 80 NQKFGKVTMTVDTSTNTAYMELSLRSEDYAVVYCARGNRFAYWGQGLTVTVSS 135

RESULT 11

US-09-355-925-7
; Sequence 7, Application US/09355925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of H chain V region version r of
; OTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7

Query Match 81.0%; Score 363.5; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 9.5e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW-----43

Db 20 QVQLVQSGAEVKKPGASVKVSCKASGYTTPYMQWVRQAPGQGLEWMSIFPGDGTRY 79

QY 44 -----GKATLVDKSTSTAYMELSLRSEDYAVFCAR-----WGQGTIVTVSS 87

Db 80 SQKFKGRVTMTADKSTSTAYMELSLRSEDYAVVYCARGLRGGYFDYWGQGTIVTVSS 139

RESULT 12

US-09-355-925-8
; Sequence 8, Application US/09355925
; Patent No. 6503510
; GENERAL INFORMATION:
; APPLICANT: KOISHIHARA, YASUO
; APPLICANT: YOSHIMURA, YASUSHI
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
; FILE REFERENCE: 053466/0255
; CURRENT APPLICATION NUMBER: US/09/355,925
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/JP98/00568
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: JP 9-41410
; PRIOR FILING DATE: 1997-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence H chain V region version s of
; OTHER INFORMATION: anti-HM1.24 antibody
US-09-355-925-8

Query Match 81.0%; Score 363.5; DB 4; Length 139;
Best Local Similarity 62.5%; Pred. No. 9.5e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 33; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVRVSKASGYST-----WVRQSPGKGLEW-----43

Db 20 QVQLVQSGAEVKKPGASVKSCASGYTFPTYNMQWVRQAPGQGLEWVGSIFFPGDGTTRY 79
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTIVTVSS 87
Db 80 SQKFKGRVTITADKSTSTAYMELSLRSEDYAVYFCARGLRGYVFDYWGQGTIVTVSS 139

RESULT 13
US-08-561-521-41
; Sequence 41, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01219-41

Query Match 80.7%; Score 362.5; DB 2; Length 116;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVVRVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 43
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFKGVTMTVDSTNTAYMELSLRSEDYAVYFCARGNRFAYWGQGLTVTVSS 116

US-08-561-521-41

Query Match 80.7%; Score 362.5; DB 2; Length 116;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVVRVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 43
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFKGVTMTVDSTNTAYMELSLRSEDYAVYFCARGNRFAYWGQGLTVTVSS 116

RESULT 14
PCT-US95-01219-41
; Sequence 41, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-41

Query Match 80.7%; Score 362.5; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4; Indels 29; Gaps 3;

QY 1 QIQLVQSGGEVKKPGASVVRVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 43
Db 1 QVQLVQSGAEVKKPGASVKVSKASGYSTFTSYIHWVRQAPGQGLEWVIDPFGNGTSY 60

QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTIVTVSS 87
Db 61 NQKFKGVTMTVDSTNTAYMELSLRSEDYAVYFCARGNRFAYWGQGLTVTVSS 116

RESULT 15
US-08-458-516-10
; Sequence 10, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458.516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059.159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal fragment
US-08-458-516-10

Query Match 80.2%; Score 360; DB 1; Length 119;
Best Local Similarity 63.0%; Pred. No. 1.9e-30;
Matches 75; Conservative 9; Mismatches 3; Indels 32; Gaps 3;
QY 1 QIQLVQSGGEVKKPGASVRSCKASGYST-----WYRQSPFGKLEWI----- 43
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGYFTNYLIEWVRQAPGQGLEWIGVYPGSGGTNY 60
QY 44 -----GKATLTVDKSTSTAYMELSLRSEDYAVYFCAR-----WGQGTITVTVSS 87
Db 61 NEKFKGRVTLTVDESTNTAYMELSLRSEDYAVYFCARRDGNYGWFAYWGQGTITVTVSS 119

Search completed: January 13, 2004, 12:46:33
Job time : 8.52227 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 7.75633 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553
Sequence: 1 RTVAAPSVFIFFPPSDQLKLS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0244	Ig kappa chain NIG
2	553	100.0	215	2 JE0242	Ig kappa chain NIG
3	553	100.0	215	2 JE0243	Ig kappa chain NIG
4	550	99.5	135	2 S02059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-I
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 K1RTB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain V-C
13	359	64.9	106	1 K1RTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain - m
17	352	63.7	218	2 JC5810	monoclonal antibody
18	352	63.7	219	2 FC4203	Ig kappa chain (mo
19	352	63.7	219	2 S16112	Ig kappa chain V r
20	352	63.7	219	2 S52028	Ig kappa chain - m
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 K1MS	Ig kappa chain C r
27	350	63.3	126	2 I54782	gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JLO029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

Ig kappa chain (Ma
Ig kappa chain V r
Ig kappa-B4 chain
Ig kappa-2 chain C
Ig kappa chain pre
Ig kappa-B4 chain
Ig kappa-1 chain C
Ig kappa-B9 chain
Ig lambda-like cha
Ig kappa chain C r
Ig lambda chain J-C re
Ig lambda chain C
Ig light chain pre
Ig light chain C r
Ig kappa-B5 chain
Ig kappa chain (WM

ALIGNMENTS

RESULT 1
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
R:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL am
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFFPPSDQLKLSGTASVVCLLNNFFPRKQVQKVDNALQSGNSQESVTEQD 60
Db 109 RTVAAPSVFIFFPPSDQLKLSGTASVVCLLNNFFPRKQVQKVDNALQSGNSQESVTEQD 168
Qy 61 SKDSTVSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 107
Db 169 SKDSTVSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
R:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, J
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e-47;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFFPPSDQLKLSGTASVVCLLNNFFPRKQVQKVDNALQSGNSQESVTEQD 60
Db 109 RTVAAPSVFIFFPPSDQLKLSGTASVVCLLNNFFPRKQVQKVDNALQSGNSQESVTEQD 168

A;Contents: annotation
A;Gene: GDB:10KC
A;Cross-references: GDB:120086; OMIM:147200
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds, in some cases, such as IgA and IgM, the subunits associate into larger complexes with heavy chain disulfide bonds; immunoglobulin homology
C;Superfamily: heterotrimer; immunoglobulin
C;Keywords: heterotrimer; immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
F;25-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61
DB 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 KSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6
JE0241
Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alim, M.A.; Yanaka, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0241
A;Molecule type: protein
A;Residues: 1-216 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;
Best Local Similarity 97.2%; Pred. No. 9.9e-46;
Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 110 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 170 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A;Reference number: A23746; MUID:9131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;
Best Local Similarity 98.1%; Pred. No. 4.7e-44;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 109 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGE 106
DB 169 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGE 214

RESULT 8
A37927
Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
C;Accession: A37927
R;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
Am. J. Hum. Genet. 48, 613-620, 1991
A;Title: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
A;Accession: A37927
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-99 <KUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;
Best Local Similarity 99.0%; Pred. No. 9e-44;
Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 68
DB 1 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 60

QY 69 SSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9
S26653
Ig kappa chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 19-Jul-1997 #text_change 21-Jan-2000
C;Accession: S26653
R;Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybrids 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A;Reference number: S26652; MUID:91355693; PMID:2129418
A;Accession: S26653
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-99 <EHR>
A;Cross-references: EMBL:X65287
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.5e-43;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61
DB 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTK 100

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 4.67249 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPDQLK.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	99.1	106	1 KAC HUMAN	P01834 homo sapien
2	367	66.4	106	1 KACB RAT	P01835 rattus norv
3	359	64.9	106	1 KACA RAT	P01836 rattus norv
4	350	63.3	106	1 KAC MOUSE	P01837 mus musculu
5	306.5	55.4	106	1 KACB RABIT	P01839 oryctolagus
6	257.5	46.6	103	1 KACA RABIT	P01840 oryctolagus
7	246.5	44.6	104	1 KAC9 RABIT	P01838 oryctolagus
8	241	43.6	104	1 KAC6 RABIT	P03984 oryctolagus
9	231	41.8	103	1 LAC CHICK	P20763 gallus gall
10	225	40.7	108	1 KAC RANCA	P11272 rana catesb
11	223.5	40.4	103	1 KAC5 RABIT	P01841 oryctolagus
12	210.5	38.1	105	1 LAC1 MOUSE	P01843 mus musculu
13	208.5	37.7	105	1 LAC HUMAN	P01842 homo sapien
14	203.5	36.8	105	1 LAC RABIT	P01847 oryctolagus
15	190	34.4	104	1 LAC1 RAT	P20766 rattus norv
16	187.5	33.9	213	1 IL11 HUMAN	P15814 homo sapien
17	183	33.1	104	1 LAC2 RAT	P20767 rattus norv
18	180.5	32.6	105	1 LAC PIC	P01846 sus scrofa
19	178	32.2	104	1 LAC3 MOUSE	P01845 mus musculu
20	174	31.5	104	1 LAC2 MOUSE	P01844 mus musculu
21	164.5	29.7	329	1 GC2 CAIPO	P01862 cavia porce
22	161.5	29.2	105	1 LAC5 MUSSP	P20765 mus spretus
23	157.5	28.5	421	1 EPC MOUSE	P06336 mus musculu
24	153.5	27.8	330	1 GCA4 MOUSE	P01863 mus musculu
25	153.5	27.8	339	1 GCAM MOUSE	P01865 mus musculu
26	151	27.3	326	1 GC2 HUMAN	P01859 homo sapien
27	151	27.3	327	1 GC4 HUMAN	P01861 homo sapien
28	150.5	27.2	335	1 GC4E MOUSE	P01864 mus musculu
29	149	26.9	290	1 GC3 HUMAN	P01860 homo sapien
30	148	26.8	330	1 GC1 HUMAN	P01857 homo sapien
31	146.5	26.5	105	1 LAC5 MOUSE	P20764 mus musculu
32	145	26.2	336	1 GCB MOUSE	P01866 mus musculu
33	145	26.2	405	1 GCBV MOUSE	P01867 mus musculu

ALIGNMENTS

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RN	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RA	(In) Fraeek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

34	143.5	25.9	323	1	GC RABIT	P01870 oryctolagus
35	143	25.9	454	1	MUC MESAU	P06337 mesocricetu
36	142.5	25.8	457	1	MUC SUNNU	P20768 suncus muri
37	141.5	25.6	429	1	EPC RAT	P01855 rattus norv
38	137.5	24.9	329	1	GCC RAT	P20762 rattus norv
39	137	24.8	324	1	GCL MOUSE	P01858 mus musculu
40	137	24.8	393	1	GCLM MOUSE	P01859 mus musculu
41	136	24.6	455	1	MUC MOUSE	P01873 mus musculu
42	136	24.6	476	1	MUCM MOUSE	P20760 rattus norv
43	135	24.4	322	1	GCA RAT	P22436 mus musculu
44	135	24.4	329	1	GC3 MOUSE	P03987 mus musculu
45	135	24.4	398	1	GC3M MOUSE	

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KACA RAT
ID AC P01836; STANDARD; PRT; 106 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region, A allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=82082587; PubMed=6273908;
RC STRAIN=DA;
RA Shepard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02118; KIRTA.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11732 MW; B7E120D970CDD66 CRC64;

Query Match 64.9%; Score 359; DB 1; Length 106;
Best Local Similarity 63.5%; Pred. No. 3 3e-29;
Matches 56; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 4 AAPSFIFFPSDQLSGTASVCLNNPYPREAKVQWKNALQSGNSQESVTQDSKD 63
Db 3 AAPTIVFIFFPSMEQLTSGGATVCFVNFYPRDISVKWIDGSEQRDGVLDSTVDQDSKD 62
QY 64 STYSLASTLTSLKADYKHKVACEVTHQGLSPVTKSNRGEC 107
Db 63 STYMSSTLSLTKEVERHNLVTCVVKHTISSPVPVKSNRNEC 106

RESULT 4
KAC_MOUSE
ID AC P01937; STANDARD; PRT; 106 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE (MOPC 21).
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
RN [2]
DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008869; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).

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RN RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing.";
RL Cell 15:1067-1075(1978).
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
RT mouse kappa immunoglobulin J' and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RT kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waale P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RT phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; V00807; CAA24189.1; -.
DR PIR; B90262; KIMS.
DR PDB; 1A1F; 01-FEB-97.
DR PDB; 1FSK; 02-OCT-00.
DR PDB; 1IGC; 03-JUN-95.
DR PDB; 1KB5; 08-APR-98.
DR PDB; 1KCB; 11-MAY-02.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCU; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96495; IGK-C.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106
SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49BAE5 CRC64;

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QY 65 TYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 63 TYNLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 103

RESULT 12
 LAC1 MOUSE STANDARD; PRT; 105 AA.
 AC P01843;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig lambda-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83014953; PubMed=6812053;
 RA Seising E., Miller J., Wilson R., Storb U.;
 RL "Evolution of mouse immunoglobulin lambda genes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
 RN [2]
 RP SEQUENCE FROM N.A. (MOPC 315).
 RX MEDLINE=81148806; PubMed=6259534;
 RA Bothwell A.L.M., Faskind M., Schwartz R.C., Sonenshein G.E.,
 RA Gelfer M.L., Baltimore D.;
 RL "Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
 RT Nature 290:65-67(1981).
 RN [3]
 RP SEQUENCE FROM N.A. (S43).
 RX MEDLINE=82220143; PubMed=6283385;
 RA Bothwell A.L.M., Faskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RL "Somatic variants of murine immunoglobulin lambda light chains.";
 RT Nature 288:380-382(1982).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
 RX MEDLINE=71107854; PubMed=5276767;
 RA Appella E.;
 RL "Amino acid sequences of two mouse immunoglobulin lambda chains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 69:590-594(1971).
 CC -1- MISCELLANEOUS: The MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
 CC NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAT IS MISSING
 CC A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
 CC APPEARS COMPLETELY NORMAL.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 CC
 CC EMBL; J00582; AAA51636.1; -
 CC EMBL; J00587; AAB59672.1; -
 CC PIR; A93922; LIMS.
 CC PDB; 1JNH; 06-FEB-02.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig-cl.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00407; IGC1; 1.
 CC PROSITE; PS00835; IG_LIKE; 1.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 KW
 FT NON_TER 1
 FT DOMAIN 6 100 IG-LIKE.
 FT DISULFID 27 86

FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
 FT CONFLICT 19 20 ET -> TE (IN REF. 4).
 FT CONFLICT 56 56 Q -> E (IN REF. 4).
 FT CONFLICT 75 75 MISSING (IN REF. 4).
 FT CONFLICT 81 82 HS -> SH (IN REF. 4).
 FT CONFLICT 85 85 S -> SS (IN REF. 4).
 FT CONFLICT 96 96 E -> Q (IN REF. 4).
 SQ SEQUENCE 105 AA; 11575 MW; A89F2B09BCFCA018 CRC64;

Query Match 38.1%; Score 210.5; DB 1; Length 105;
 Best Local Similarity 42.5%; Pred. No. 2.2e-14;
 Matches 45; Conservative 20; Mismatches 34; Indels 7; Gaps 3;

QY 4 AAPSVPFPPSDQLKSGTASVVLNNFVREARKVQWKVDNALQSGNSQESVTEQDSK 63
 DB 4 SSPSVTLTLPSSSELETKALVLTITDFPGVTVVDWKVDG---TPVTQGMETQPSKQ 60
 QY 64 ST--YSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SNNKYMASSVLTLTARAWERHSSVSCQVTHEG--HTVEKSLSRADC 104

RESULT 13
 LAC1 HUMAN STANDARD; PRT; 105 AA.
 AC P01842; P80423;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig lambda chain C regions.
 GN IGLC1 AND IGLC2 AND IGLC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN SH).
 RX MEDLINE=70165723; PubMed=4909564;
 RA Titani K., Wikler M., Shinoda T., Putnam F.W.;
 RL "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
 RL complete amino acid sequence and the location of the disulfide
 RL bridges.";
 RL J. Biol. Chem. 245:2171-2176(1970).
 RN [2]
 RP SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
 RX MEDLINE=69088380; PubMed=4883841;
 RA Milstein C., Clegg J.B., Jarvis J.M.;
 RL "Immunoglobulin lambda-chains. The complete amino acid sequence of a
 RL Bence-Jones protein.";
 RL Biochem. J. 110:631-652(1968).
 RN [3]
 RP SEQUENCE (BENCE-JONES PROTEIN NIG-64).
 RX MEDLINE=83186114; PubMed=6404900;
 RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
 RA Shimizu A.;
 RL "Comparative studies on the structure of the light chains of human
 RL immunoglobulins IV. Assignment of a subgroup.";
 RL J. Biochem. 93:421-429(1983).
 RN [4]
 RP SEQUENCE (BENCE-JONES PROTEIN KERN).
 RX MEDLINE=71150336; PubMed=5549568;
 RA Ponstingl H., Hess M., Hilschmann N.;
 RL "Structural rule of antibodies. Primary structure of a monoclonal
 RL immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-
 RL protein Kern). V. The complete amino acid sequence and its genetic
 RL interpretation.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971).
 RN [5]
 RP PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
 RX MEDLINE=74109253; PubMed=4814727;
 RA Chen B.I., Poljak R.J.;
 RL "Amino acid sequence of the (lambda) light chain of a human myeloma
 RL immunoglobulin (19G New).";

immunoglobulin lambda-chains.";
Biochem. J. 197;177-183(1981).
-1- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC SPECIFICITY.
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 6 100 IG-LIKE.
FT DISULFID 27 86
FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;
Query Match 36.8%; Score 203.5; DB 1; Length 105;
Best Local Similarity 44.3%; Pred. No. 1.1e-13;
Matches 47; Conservative 15; Mismatches 33; Indels 11; Gaps 4;
QY 6 PSVIFPPSDEQLKSGTASVCLANNFYPREAKVQWKVDNALQSGNS--QESVTEQDSK 63
DB 6 PSVILFPSPSEELKONKATLVCLISDFPRVYKWKAD-----GNSVTQGVDTTPSKQ 60
QY 64 ST--YSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SNKYAASSFLHTANQWKSQSVTCQVTHG--HTVEKSLAPABC 104
SEQUENCE FROM N.A.
RX MEDLINE=87305594; PubMed=3114047;
RA Steen M.L., Hellman L., Pettersson U.;
RT "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
RL Gene 55:75-84(1987).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; M22520; AAA41419.1; ALT_INIT.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT 1

FT DOMAIN 6 99 IG-LIKE.
FT DISULFID 27 85
FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
SQ SEQUENCE 104 AA; 11565 MW; CBF71811F4BC978A CRC64;
Query Match 34.4%; Score 190; DB 1; Length 104;
Best Local Similarity 39.0%; Pred. No. 2.4e-12;
Matches 41; Conservative 20; Mismatches 38; Indels 6; Gaps 3;
QY 4 AAPSVEIFPPSDEQLKSGTASVCLANNFYPREAKVQWKVDNA-LQSGNSQSVTEQDSK 62
DB 4 ATPSVTLFPSPSEELKTDKATLVCMVTDYFGVMTVWKADGTPITQGVETTPQPKQNNK 63
QY 63 DSTYLSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 107
DB 64 ---YNATSYLLITAKAWETHSNYSQOVTHE--ENTVEKSLRAEC 103
Search completed: January 13, 2004, 12:39:27
Job time : 5.67249 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 19.1572 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFIFPPSDEQLKLS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_todent:*

12: sp_virus:*

13: sp_vertibrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	234	4 Q8NEK1	Q8nek1 homo sapien
2	553	100.0	239	4 Q8TCD0	Q8tcd0 homo sapien
3	549	99.3	239	4 Q8NEK0	Q8nek0 homo sapien
4	352	63.7	233	11 Q91WS9	Q91ws9 mus musculus
5	352	63.7	234	11 Q8R028	Q8r028 mus musculus
6	352	63.7	234	11 Q91W88	Q91w88 mus musculus
7	352	63.7	234	11 Q8R062	Q8r062 mus musculus
8	352	63.7	234	11 Q8VC60	Q8vc60 mus musculus
9	352	63.7	235	11 Q91W12	Q91w12 mus musculus
10	352	63.7	238	11 Q8VC16	Q8vc16 mus musculus
11	352	63.7	238	11 Q99M37	Q99m37 mus musculus
12	352	63.7	239	11 Q8VC55	Q8vc55 mus musculus
13	352	63.7	239	11 Q8K058	Q8k058 mus musculus
14	347	62.7	214	11 Q8R1A5	Q8r1a5 mus musculus
15	211.5	38.2	106	4 Q8TCJ5	Q8tcj5 homo sapien
16	211.5	38.2	233	4 Q8TBC9	Q8tbc9 homo sapien

17	211.5	38.2	236	4 Q8NEJ1	Q8nej1 homo sapien
18	210.5	38.1	130	11 Q9D8W4	Q9d8w4 mus musculus
19	208.5	37.7	233	4 Q8N5F4	Q8n5f4 homo sapien
20	208.5	37.7	234	4 Q8N355	Q8n355 homo sapien
21	208.5	37.7	237	4 Q8WUK4	Q8wuk4 homo sapien
22	208.5	37.7	237	4 Q8WTU6	Q8wtu6 homo sapien
23	208.5	37.7	240	4 Q8WUK3	Q8wuk3 homo sapien
24	199.5	36.1	235	11 Q99M11	Q99m11 mus musculus
25	192.5	34.8	233	4 Q96I69	Q96i69 homo sapien
26	192.5	34.8	236	4 Q96E61	Q96e61 homo sapien
27	174	31.5	105	11 Q99JC1	Q99jc1 mus musculus
28	159.5	28.8	473	11 Q9D8L4	Q9d8l4 mus musculus
29	153.5	27.8	468	11 Q99L31	Q99l31 mus musculus
30	153.5	27.8	473	11 Q99L25	Q99l25 mus musculus
31	151	27.3	473	4 Q8TC63	Q8tc63 homo sapien
32	149	26.9	509	4 Q8NF17	Q8nf17 homo sapien
33	149	26.9	521	4 Q8N4Y9	Q8n4y9 homo sapien
34	148	26.8	471	4 Q8TC77	Q8tc77 homo sapien
35	148	26.8	701	4 Q96PQ8	Q96pq8 homo sapien
36	144	26.0	473	11 Q91Z05	Q91z05 mus musculus
37	144	26.0	474	11 Q8R3H6	Q8r3h6 mus musculus
38	143	25.9	463	11 Q99LC4	Q99lc4 mus musculus
39	142	25.7	437	11 Q9R1A4	Q9r1a4 mus musculus
40	142	25.7	469	11 Q8R3V9	Q8r3v9 mus musculus
41	139.5	25.2	337	6 Q95M34	Q95m34 equus caball
42	136	24.6	613	11 Q8VCX7	Q8vcx7 mus musculus
43	134	24.2	684	13 Q90544	Q90544 ginglymosto
44	127.5	23.1	267	13 Q90529	Q90529 ginglymosto
45	127.5	23.1	268	13 Q90524	Q90524 ginglymosto

ALIGNMENTS

RESULT 1

Q8NEK1	PRELIMINARY;	PRT;	234 AA.
ID	Q8NEK1		
AC	Q8NEK1;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	Strausberg R.;		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC030813; AAH30813.1; -		
DR	InterPro; IPR007110; IG-like.		
DR	InterPro; IPR003597; IG-cl.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR003596; IG_v.		
DR	Pfam; PF00047; ig, 2.		
DR	SMART; SM00407; IGI; 1.		
DR	SMART; SM00406; IGI; 1.		
DR	PROSITE; PS00835; IG LIKE; 2.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KW	Hypothetical protein.		
SK	SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;		

Query Match 100.0%; Score 553; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFPPSDEQLKLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 128 RTVAAPSVFIFPPSDEQLKLSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187

Qy 61 SKDSTVLSLTSLKADYKHKVACEVTHOGLSPVTKSFNRGEC 107

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028540; AAH28540.1; --
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25702 MW; 148377F9C1CDOAEE CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 6

Q91WFB PRELIMINARY; PRT; 234 AA.
 AC Q91WFB;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 25.9 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015292; AAH15292.1; --
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR InterPro; IPR001865; Ribosomal_s2.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS00982; RIBOSOMAL_s2_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B056EB7812D2 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 7

Q8R062 PRELIMINARY; PRT; 234 AA.
 AC Q8R062;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 25.9 kDa protein.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027418; AAH27418.1; --
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60
 DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 8

Q8VCP0 PRELIMINARY; PRT; 234 AA.
 AC Q8VCP0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 25.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019474; AAH19474.1; --
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.

QY 1 RTVAAPSVFPPSPDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQD 60

DB 128 RADAAPTQSVIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQD 187

QY 61 SKDSTYSLSTLTLSKADYEKKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 188 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNRNEC 234

RESULT 9

Q91W12 PRELIMINARY; PRT; 234 AA.

```
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTIVFPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTVSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 107
DB 193 SKDSTYSMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 239

RESULT 13
Q8KOF8 PRELIMINARY; PRT; 239 AA.
ID Q8KOF8
AC Q8KOF8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue-Breast tumor;
RA Strausberg K.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00230; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTIVFPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTVSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 107
DB 193 SKDSTYSMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 239

RESULT 14
Q9RIA5 PRELIMINARY; PRT; 214 AA.
ID Q9RIA5
AC Q9RIA5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
```

```
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1 214
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 62.7%; Score 347; DB 11; Length 214;
Best Local Similarity 59.8%; Pred. No. 3.9e-28;
Matches 64; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
QY 1 RTVAAPSVFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RADAAPTIVFPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNSWTDQD 167
QY 61 SKDSTVSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 107
DB 168 SKDSTYSMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 214

RESULT 15
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
ID Q8TCJ5
AC Q8TCJ5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (fragment).
GN DKFZP667J0810.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Lymph node;
RA Duisterhoef A.; Lauber J.; Mewes H.W.; Weil B.; Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00407; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 106 106
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 38.2%; Score 211.5; DB 4; Length 106;
Best Local Similarity 41.0%; Pred. No. 2e-14;
Matches 43; Conservative 26; Mismatches 31; Indels 5; Gaps 3;
QY 4 AAPSFTVFPSSDQLKSGTASVVCCLNNFYPREAKVQWKVDNA-LOGNSQESVTEQDSK 62
DB 5 AAPSFTVFPSSDQLKSGTASVVCCLNNFYPREAKVQWKVDNA-LOGNSQESVTEQDSK 62
QY 63 DSTVSLSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 107
DB 63 NKYAASSLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTEC 105

Search completed: January 13, 2004, 12:43:08
Job time : 20.1572 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 24.9511 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-97
Perfect score: 553
Sequence: 1 RRVAPSVFIPPSDEQLKS.....EVTHQGLSSPVTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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22: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
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24: /SIDSI/gcgdata/geneseq/geneseq-embl/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	19 AAW40578	Human kappa CL dom
2	553	100.0	107	20 AAY50152	Human kappa light
3	553	100.0	107	20 AAY08745-	Human kappa-CL dom
4	553	100.0	107	20 AAW92425	Human kappa protei
5	553	100.0	107	21 AAB27000	Human kappa CL dom
6	553	100.0	107	23 ABB31883	Human kappa CL dom
7	553	100.0	107	24 ABB98755	Human kappa light
8	553	100.0	143	10 RAFP9359	Sequence of human
9	553	100.0	193	22 AAW52145	Humanised HMFG1 li

10	553	100.0	201	20 AAY29770	P-selectin ligand
11	553	100.0	212	23 ABP51955	Humanised anti-CD1
12	553	100.0	213	17 AAW04301	Antibody fusion pr
13	553	100.0	213	22 AAE10510	Humanised high pot
14	553	100.0	213	22 AAE10512	Humanised high pot
15	553	100.0	213	22 AAE10514	Humanised high pot
16	553	100.0	213	22 AAE10516	Humanised high pot
17	553	100.0	213	22 AAE10518	Humanised high pot
18	553	100.0	213	22 AAE10520	Humanised high pot
19	553	100.0	213	22 AAE10522	Humanised high pot
20	553	100.0	213	22 AAE10524	Humanised high pot
21	553	100.0	213	22 AAE10526	Humanised high pot
22	553	100.0	213	22 AAB83157	Ganglioside GM2 an
23	553	100.0	213	23 ABP66563	Human RSV antibody
24	553	100.0	213	23 ABP66565	Human RSV antibody
25	553	100.0	213	23 ABP66567	Human RSV antibody
26	553	100.0	213	23 ABP66569	Human RSV antibody
27	553	100.0	213	23 ABP66571	Human RSV antibody
28	553	100.0	213	23 ABP66573	Human RSV antibody
29	553	100.0	213	23 ABP66575	Human RSV antibody
30	553	100.0	213	23 ABP66577	Human RSV antibody
31	553	100.0	213	23 ABP66579	Human RSV antibody
32	553	100.0	213	23 ABP66581	Human RSV antibody
33	553	100.0	213	23 ABP66583	Human RSV antibody
34	553	100.0	213	23 ABP66585	Human RSV antibody
35	553	100.0	213	23 ABP66587	Human RSV antibody
36	553	100.0	213	23 ABP66589	Human RSV antibody
37	553	100.0	213	23 ABP66591	Human RSV antibody
38	553	100.0	213	23 ABP66593	Human RSV antibody
39	553	100.0	213	23 ABP66595	Human RSV antibody
40	553	100.0	213	23 ABP66597	Human RSV antibody
41	553	100.0	213	23 ABP66599	Human RSV antibody
42	553	100.0	213	23 ABP66601	Human RSV antibody
43	553	100.0	213	23 ABP66605	Human RSV antibody
44	553	100.0	213	23 ABP66607	Human RSV antibody
45	553	100.0	213	23 ABP66609	Human RSV antibody

ALIGNMENTS

RESULT 1

AAW40578
ID AAW40578 standard; protein; 107 AA.

AC AAW40578;

XX

XX

DT 21-JUL-1998 (first entry)

XX Human kappa CL domain protein fragment.

DE

XX Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;

KW disorder; salvage receptor binding epitope; cell adherence interaction;

KW lymphocyte; T cell inflammatory response.

XX

OS Homo sapiens.

XX

PN US5739277-A.

XX

PD 14-APR-1998.

XX

PF 14-APR-1995; 95US-0422101.

XX

PR 14-APR-1995; 95US-0422101.

XX (GETH) GENENTECH INC.

XX

PA

XX

PI Presta LG, Snedecor BR;

XX

XX WPI; 1998-250490/22.

DR

XX Polypeptide(s) that are not Fc fragments and have an increased

XX half-life - are useful for the treatment of LFA-1 mediated disorders

PT

XX Disclosure; Fig 4A-B; 25pp; English.

PS This invention describes a method for improving the clinical outcome in

CC focal ischaemic stroke by administering novel anti-CD18 antibody which

CC has cerebroprotective properties. The invention particularly describes a

CC method of treating focal ischaemic stroke caused by the obstruction of a

CC main cerebral artery which comprises administering an anti-CD18 antibody

CC to increase the blood flow or reduce the infarct size, where: (1) the

CC antibody binds to an extracellular domain of CD18 and inhibits or reduces

CC the ability of the cell expressing CD18 to bind to endothelium, (2) the

CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the

CC antibody dissociates CD18/CD18 complex. This sequence represents the

CC human kappa-CL domain which is used to illustrate the method of the

CC invention.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 20; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49; Indels 0; Gaps 0;

XX Matches 107; Conservative 0; Mismatches 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4

ID AAW92425 standard; peptide; 107 AA.

XX AAW92425;

XX 23-APR-1999 (first entry)

XX Human Kappa protein CL domain.

XX Antibody; salvage receptor binding epitope; Fab; F(ab')₂; immunoglobulin;

XX CH region; CL region; kidney; Fc region; CH1 domain; CH2 domain; Igg;

XX kappa protein; renal clearance rate; circulatory half-life.

XX Homo sapiens.

XX US5869046-A.

XX 09-FEB-1999.

XX 14-APR-1995; 95US-0422092.

XX 14-APR-1995; 95US-0422092.

XX (GETH) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 1999-152694/13.

XX Production of antibody fragments with reduced renal clearance - by

XX introducing salvage receptor binding epitope into CH1 or CL region.

XX Disclosure; Column 55-58; 38pp; English.

PS This invention describes a method for preparing a variant Fab or F(ab')₂

CC polypeptide having increased half-life in vivo, where the polypeptide

CC contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is

CC cleared from the kidneys and does not contain an Igg Fc region. The

CC method involves altering the polypeptide within the CH1 or CL region to

CC incorporate a salvage receptor binding epitope taken from two loops of

CC a CH2 domain of an Igg Fc region. The polypeptides have a reduced renal

CC clearance rate and an increased circulatory half-life. This sequence

CC represents a human kappa protein CL domain used in the method of the

CC invention.

XX Sequence 107 AA;

XX Query Match 100.0%; Score 553; DB 20; Length 107;

XX Best Local Similarity 100.0%; Pred. No. 6.4e-49; Indels 0; Gaps 0;

XX Matches 107; Conservative 0; Mismatches 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

DB 61 SKDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5

ID AAB27000 standard; Protein; 107 AA.

XX AAB27000;

XX 25-JAN-2001 (first entry)

XX Human kappa CL domain.

XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;

XX mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;

XX psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;

XX inflammation; vaccine.

XX Homo sapiens.

XX US6121022-A.

XX 19-SEP-2000.

XX 14-APR-1995; 95US-0422112.

XX 14-APR-1995; 95US-0422112.

XX (GETH) GENENTECH INC.

XX Presta LG, Snedecor BR;

XX WPI; 2000-610925/58.

XX New nucleic acid encoding new modified polypeptides with increased

XX circulatory half-life useful for preventing/treating LFA-1-mediated

XX disorders, e.g. reducing inflammatory responses or inducing tolerance

XX to immunostimulants -

XX Disclosure; Fig 2; 38pp; English.

XX The present sequence was used in a method for improving the in vivo

XX half-life of polypeptides. The polypeptides comprise an Ig constant

XX domain or an Ig-like constant domain, and a salvage receptor binding

XX epitope within the Ig or Ig-like domain. The salvage receptor epitope is

XX taken from two loops of the CH2 domain of an Fc region of an Ig molecule.

XX The modified polypeptides are useful for preventing or treating

XX LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis,

XX allergic conditions (e.g. eczema), antigen-antibody complex mediated,

XX diseases, B-cell lymphomas. They are also useful for wound repair,

XX reducing inflammatory responses and inducing tolerance to

XX immunostimulants. They may also be used in diagnostic assays. The nucleic

XX acids and modified polypeptides are useful for the passive immunisation

XX of patients, as well as for affinity purification of an antigen from

XX recombinant cell culture or natural sources.

XX Sequence 107 AA;

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8

AAP93559
 ID AAP93559 standard; protein; 143 AA.

AC AAP93559;
 XX 25-MAR-2003 (updated)
 DT 28-JAN-1991 (first entry)
 XX Sequence of human kappa light chain fragment.

XX HIV; antiviral; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..37
 FT /label=
 FT /note="light variable and joining"
 FT Region 38..38
 FT /note="light constant"
 FT Region 37..38
 FT /note="insert site"

XX WO8902922-A.

XX 06-APR-1989.

XX 03-OCT-1988; 88WO-US03414.

XX 02-OCT-1987; 87US-0104329.

XX 28-SEP-1988; 88US-0250785.

XX (GETH) GENENTECH INC.

XX Capon DJ, Gregory TJ;

XX WPI; 1989-114397/15.

XX P-PSDB; AAP93559.

XX New nucleic acid sequences encoding adhesin, esp. CD4, variants -
 PT partic. with trans-membrane domain inactivated or fused to other
 PT peptide, useful esp. for treating HIV infections

XX Example; Figure Fig 5; 79pp; English.

XX It is employed in the prepn. of CD4 fusions. The insert site is
 CC given in the Features Table. CD4 fusion proteins can have antiviral and
 CC immunomodulatory activity are esp. useful for treating HIV infections,
 CC regardless of genetic variation within the virus. They and antibodies
 CC raised against them can also be used diagnostically for assaying adhesions
 CC and their ligands.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 143 AA;

Query Match 100.0%; Score 553; DB 10; Length 143;
 Best Local Similarity 100.0%; Pred. No. 9.2e-49;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 37 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 96

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 97 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 143

RESULT 9

AAM52145
 ID AAM52145 standard; Protein; 193 AA.

AC AAM52145;

XX 05-FEB-2002 (first entry)

XX Humanised HMFG1 light chain.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

XX cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX Synthetic.

XX WO200174905-A1.

XX 11-OCT-2001.

XX 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

XX 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOWA RES LTD.

XX Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion

XX comprising humanised monoclonal antibody having specificity for

XX polymorphic epithelial mucin, and cytotoxic portion having

XX endonucleolytic activity

XX Claim 20; Figure 3; 176pp; English.

XX The invention relates to a compound which comprises a target

XX cell-specific portion, comprising an humanised monoclonal antibody,

XX having specificity for polymorphic epithelial mucin (PEM) or its antigen

XX binding fragment and a cytotoxic portion having endonucleolytic activity,

XX exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The

XX compound has cytostatic activity useful for treating cancer and acting as

XX a potential inducer of apoptosis.

XX Sequence 193 AA;

Query Match 100.0%; Score 553; DB 22; Length 193;

Best Local Similarity 100.0%; Pred. No. 1.3e-48;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 87 RTVAAPSVFIFFPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 146

QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 107

DB 147 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSSPVTKSFNRGEC 193

RESULT 10

AAY29770
 ID AAY29770 standard; Protein; 201 AA.

AC AAY29770;

XX 04-NOV-1999 (first entry)

XX P-selectin ligand and kappa chain constant region fusion protein.

XX Human; P-selectin ligand; glycoprotein; fusion protein; infection;

```
Db 106 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 12
AAW04301
ID AAW04301 standard; Protein; 213 AA.
XX
AC AAW04301;
XX
XX 25-MAR-2003 (updated)
DT 14-FEB-1997 (first entry)
XX
DE Antibody fusion protein.
XX
KW Antibody; fusion protein; recombinant antibody; tumour therapy;
KW prodrug.
XX
OS Synthetic.
XX
PN EP737747-A2.
XX
PD 16-OCT-1996.
XX
PF 13-MAR-1996; 965EP-0103913.
XX
PR 11-APR-1995; 95DE-1013676.
XX
PA (BEHW ) BEHRINGWERKE AG.
XX
PI Bosslet K, Czech J, Oppen M;
XX
XX WPI; 1996-457328/46.
DR N-PSDB; AAT38397.
XX
XX Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion
PT protein - by cytoplasmic expression in thio:redoxin:reductase
PT deficient E. coli
XX
XX Example 1; Figure 5a; 12pp; German.
XX
XX Production of recombinant antibodies (Ab), Ab fragments or Ab
XX fragment/enzyme fusion proteins can be used for tumour therapy,
XX especially when the fusion protein comprises a tumour-specific
XX Ab fragment and an enzyme capable of converting a non-toxic prodrug
XX to a toxic drug. The fusion proteins are constructed in expression
XX vectors and expressed in thio:redoxin:reductase deficient E.coli,
XX allowing expression products to be isolated in soluble functional
XX form without renaturation. The Ab fragment is an Fab fragment or an
XX antigen binding region. In the fusion protein, the Ab component is
XX humanised and the enzyme component is a human cytoplasmic enzyme.
XX This fusion protein comprises the antibody constant and variable
XX light chain regions.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 17; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
AAE10512
ID AAE10512 standard; Protein; 213 AA.
XX
AC AAE10512;
XX
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RESULT 13
AAE10510
ID AAE10510 standard; Protein; 213 AA.
XX
AC AAE10510;
XX
DT 10-DEC-2001 (first entry)
XX
XX Humanised high potency antibody clone 25 full length light chain.
XX
KW Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200164751-A2.
XX
PD 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US06815.
XX
XX 01-MAR-2000; 2000US-0186252.
XX
XX (MEDI-) MEDIMUNE INC.
XX
XX Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX WPI; 2001-582150/65.
XX
XX High potency recombinant antibody, useful for preventing and treating
XX diseases induced or caused by viruses, especially respiratory syncytial
XX virus and parainfluenza virus, has high kinetic association rate
XX constant -
XX
XX Claim 23; Page 75-76; 98pp; English.
XX
XX The invention relates to a high potency antibody including its
XX immunologically active portions, fragments and segments other than
XX vitamin. The antibody has increased potency, high rate constant for
XX antibody-antigen complex formation and high affinity for any desired
XX antigen. The high potency antibody is also useful for nullifying or
XX ameliorating the effects of addictive drugs, such as cocaine. The high
XX potency has specificity for antigenic determinants found on microbes
XX such as viruses, bacteria or fungi, antigens found on cancer cells and
XX toxic substances or product of toxic substances. The high potency
XX antibody is useful for preventing or treating a disease caused by a
XX virus such as respiratory syncytial virus (RSV) and parainfluenza
XX virus (PIV). The present sequence is humanised high potency antibody
XX full length light chain variable region.
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 22; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
AAE10512
ID AAE10512 standard; Protein; 213 AA.
XX
AC AAE10512;
XX
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 17.1013 Seconds
(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-97

Perfect score: 553

Sequence: 1 RTVAAPSVFPPRDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	553	100.0	107	11	US-09-990-586-97
3	553	100.0	107	11	US-09-990-586-99
4	553	100.0	107	12	US-10-159-006-20
5	553	100.0	107	12	US-10-310-113-166
6	553	100.0	107	12	US-10-310-113-168
7	553	100.0	107	12	US-10-230-880-97
8	553	100.0	107	12	US-10-230-880-99
9	553	100.0	107	15	US-10-366-709-54
10	553	100.0	107	15	US-10-121-464-18
11	553	100.0	107	15	US-10-269-805-67
12	553	100.0	212	12	US-10-320-231A-77
13	553	100.0	212	14	US-10-011-125-5
14	553	100.0	213	9	US-09-796-848A-38
15	553	100.0	213	9	US-09-796-848A-40

16	553	100.0	213	9	US-09-796-848A-42
17	553	100.0	213	9	US-09-796-848A-44
18	553	100.0	213	9	US-09-796-848A-46
19	553	100.0	213	9	US-09-796-848A-48
20	553	100.0	213	9	US-09-796-848A-50
21	553	100.0	213	9	US-09-796-848A-52
22	553	100.0	213	9	US-09-796-848A-54
23	553	100.0	213	10	US-09-996-288-209
24	553	100.0	213	10	US-09-996-288-211
25	553	100.0	213	10	US-09-996-288-213
26	553	100.0	213	10	US-09-996-288-215
27	553	100.0	213	10	US-09-996-288-217
28	553	100.0	213	10	US-09-996-288-219
29	553	100.0	213	10	US-09-996-288-221
30	553	100.0	213	10	US-09-996-288-223
31	553	100.0	213	10	US-09-996-288-225
32	553	100.0	213	10	US-09-996-288-227
33	553	100.0	213	10	US-09-996-288-229
34	553	100.0	213	10	US-09-996-288-231
35	553	100.0	213	10	US-09-996-288-233
36	553	100.0	213	10	US-09-996-288-235
37	553	100.0	213	10	US-09-996-288-237
38	553	100.0	213	10	US-09-996-288-239
39	553	100.0	213	10	US-09-996-288-241
40	553	100.0	213	10	US-09-996-288-243
41	553	100.0	213	10	US-09-996-288-245
42	553	100.0	213	10	US-09-996-288-247
43	553	100.0	213	10	US-09-996-288-251
44	553	100.0	213	10	US-09-996-288-253
45	553	100.0	213	10	US-09-996-288-255

ALIGNMENTS

RESULT 1

US-09-811-384-5
; Sequence 5, Application US/09811384
; Patent No. US20020081294A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; Thomas, G. Roger
; Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/811,384
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI729C1
; TELECOMMUNICATION INFORMATION:

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; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

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Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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RESULT 7
US-10-230-880-97
; Sequence 97, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Qy      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db      61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Db 106 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 13
US-10-011-125-5
; Sequence 5, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011.125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-5

Query Match 100.0%; Score 553; DB 14; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 14
US-09-796-848A-38
; Sequence 38, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Hexren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; TITLE OF INVENTION: Producing Them
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-38

Query Match 100.0%; Score 553; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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US-09-796-848A-40
; Sequence 40, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Hexren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; TITLE OF INVENTION: Producing Them
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-40

Query Match 100.0%; Score 553; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 RTVAAPSVFIIPPDSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

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Job time : 18.1013 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: January 13, 2004, 12:33:50 ; Search time 9.25153 seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-97
Perfect score: 553
Sequence: 1 RTVAAPSVFIPFSDQLKS.....EVTHQGLSPVTKSFNRGRC 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	553	100.0	107	1	US-08-422-091-8
3	553	100.0	107	2	US-08-422-092-8
4	553	100.0	107	2	US-08-788-800-5
5	553	100.0	107	3	US-08-422-093-8
6	553	100.0	107	3	US-08-422-112-8
7	553	100.0	107	4	US-09-301-593-20
8	553	100.0	213	3	US-08-630-820-6
9	553	100.0	213	3	US-08-397-411-12
10	553	100.0	214	1	US-08-456-516-12
11	553	100.0	214	2	US-07-934-373C-24
12	553	100.0	214	2	US-07-934-373C-39
13	553	100.0	214	2	US-07-934-373C-40
14	553	100.0	214	2	US-08-480-753-6
15	553	100.0	214	2	US-08-788-800-11
16	553	100.0	214	3	US-09-041-889-11
17	553	100.0	214	3	US-08-437-642B-24
18	553	100.0	214	3	US-08-437-642B-39
19	553	100.0	214	3	US-08-437-642B-40
20	553	100.0	214	3	US-08-837-058-11
21	553	100.0	214	3	US-09-097-309-2
22	553	100.0	214	3	US-08-397-411-5
23	553	100.0	214	3	US-09-097-171A-2
24	553	100.0	214	4	US-09-247-352-4
25	553	100.0	214	4	US-09-460-587-2
26	553	100.0	214	4	US-09-679-397-1
27	553	100.0	214	4	US-08-146-206C-24

28	553	100.0	214	4	US-09-466-635-4	Sequence 4, Appli
29	553	100.0	214	4	US-09-680-148-1	Sequence 1, Appli
30	553	100.0	214	4	US-09-289-942A-6	Sequence 6, Appli
31	553	100.0	214	4	US-09-304-465A-1	Sequence 1, Appli
32	553	100.0	214	4	US-09-417-264-11	Sequence 11, Appli
33	553	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appli
34	553	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appli
35	553	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appli
36	553	100.0	215	2	US-08-480-753-8	Sequence 8, Appli
37	553	100.0	218	2	US-08-887-352B-13	Sequence 13, Appli
38	553	100.0	218	2	US-08-887-352B-15	Sequence 15, Appli
39	553	100.0	218	2	US-08-887-352B-17	Sequence 17, Appli
40	553	100.0	218	2	US-08-887-352B-19	Sequence 19, Appli
41	553	100.0	218	2	US-08-887-352B-24	Sequence 24, Appli
42	553	100.0	218	3	US-08-466-151-9	Sequence 9, Appli
43	553	100.0	218	3	US-09-109-207C-13	Sequence 13, Appli
44	553	100.0	218	3	US-09-109-207C-15	Sequence 15, Appli
45	553	100.0	218	3	US-09-109-207C-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-422-101-8
; Sequence 8, Application US/08422101
; Patent No. 5739277
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.101
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RTVAAPSVFIPFSDQLKS...EVTHQGLSPVTKSFNRGRC...VTEQD 60

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-5

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-08-422-093-8
Sequence 8, Application US/08422093
Patent No. 609687;
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 932
REFERENCE/DOCKET NUMBER: 932-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-422-093-8

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A

Qy	1	RTVAAPSFTI	PPPSDEQL	KSQTASV	VVCLLN	NFPY	PREAKV	QKV	VDNAL	QSGS	QESV	TEQD	60
Db	107	RTVAAPSFTI	PPPSDEQL	KSQTASV	VVCLLN	NFPY	PREAKV	QKV	VDNAL	QSGS	QESV	TEQD	166
Qy	61	SKDSTYS	LSSTLT	ISKADY	EKKHY	ACEV	THQGL	SSP	VTKS	FN	R	GEC	107
Db	167	SKDSTYS	LSSTLT	ISKADY	EKKHY	ACEV	THQGL	SSP	VTKS	FN	R	GEC	213

RESULT 10

US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 5777085

/ GENERAL INFORMATION:
 / APPLICANT: Co, Man Sung
 / APPLICANT: Tso, J. Yun
 / TITLE OF INVENTION: Humanized Antibodies Reactive with
 / TITLE OF INVENTION: GPIIB/IIIA
 / NUMBER OF SEQUENCES: 23
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: William M. Smith
 / STREET: One Market Plaza, Steuart Tower, Suite 2000
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94105

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FILING DATE: 03-MAY-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/059,159
 FILING DATE: 03-MAY-1993
 ATTORNEY/AGENT INFORMATION:

Query Match	100.0%;	Score 553;	DB 1;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 1.2e-56;		
Matches 107;	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

Qy 1 RTVAAPSVEIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Db 108 RTVAAPSVEIFPPSDEQLKSGTASVVLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167

Qy 61 SKDSTYSLSTLTLSKADYEXHKVYACEVTHQIGLSSPVTKSFNREGC 107
168 SKDSTYSLSTLTLSKADYEXHKVYACEVTHQIGLSSPVTKSFNREGC 214

RESIST 17

US-07-934-373C-24
; Sequence 24, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEC 107
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 Db 168 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEC 214
 |||||

RESULT 15

US-08-788-800-11
 ; Sequence 11, Application US/08788800
 ; Patent No. 5914112
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednar, Martin M.
 ; APPLICANT: Thomas, G. Roger
 ; APPLICANT: Gross, Cordell E.
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/788,800
 ; FILING DATE: 22-Jan-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0987r1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 214 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-788-800-11

Query Match 100.0%; Score 553; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 60
 |||||
 Db 108 RTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQGNLSQESVTEQD 167
 |||||

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEC 107
 |||||
 Db 168 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEC 214
 |||||

Search completed: January 13, 2004, 12:46:33
 Job time: 9.25153 secs

GenCore version 5.1.6
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OM: protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 24.0664 Seconds
(without alignments)
1326.564 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASFKGPSVFPLAPSSKST.....MHEALHNHYTQKSLSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76: **
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1767	99.4	330	1 GHU	Ig gamma-1 chain C
2	1630.5	91.7	377	2 A23511	Ig gamma-3 chain C
3	1528.5	91.6	377	2 A60764	Ig gamma-3 chain C
4	1604	90.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	89.5	327	1 G4HU	Ig gamma-4 chain C
6	1263.5	71.1	374	2 S69339	Ig heavy chain V r
7	1263	71.0	328	2 I47159	Ig gamma 2a chain C
8	1260	70.9	255	4 S31866	Ig gamma-1 chain C
9	1257	70.7	328	2 I47160	Ig gamma 2b chain C
10	1254	70.5	234	2 PT0207	Ig gamma chain C r
11	1231	69.2	328	2 I47158	Ig gamma 1 chain C
12	1230.5	69.2	323	1 GHXB	Ig gamma chain C r
13	1227	69.0	328	2 I47161	Ig gamma 3 chain C
14	1212.5	68.2	329	1 G2GP	Ig gamma-2 chain C
15	1199.5	67.5	472	2 S31459	Ig gamma-1 chain -
16	1180.5	66.4	470	2 S22080	Ig heavy chain pre
17	1161.5	65.3	308	2 C30554	Ig heavy chain C r
18	1154	64.9	444	2 FC4436	monoclonal antibody
19	1152	64.8	326	2 PS0017	Ig gamma-1 chain C
20	1151	64.7	289	1 G3HUI	Ig gamma-3 heavy c
21	1146.5	64.5	333	2 PS0018	Ig gamma-2b chain C
22	1142	64.2	324	1 G1MS	Ig gamma-1 chain C
23	1141	64.2	329	1 G3MSC	Ig gamma-3 chain C
24	1137	63.9	393	1 G1MSM	Ig gamma-1 chain C
25	1130	63.6	398	1 G3MSM	Ig gamma-3 chain C
26	1126	63.3	330	1 G2MSA	Ig gamma-2a chain
27	1126	63.3	469	2 S37483	Ig gamma-2a chain
28	1123.5	63.2	335	1 G2MSAB	Ig gamma-2a chain
29	1121	63.0	399	1 G2MSAM	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999

C:Accession: A93433; S38861; S33887; B90563; A90564; B91568; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers, A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S38861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113/235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer.

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <GUN>

A:Note: this sequence has the Gm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

Query Match 91.6%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 9e-107;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVPELPAPSSKSTSGTAALGCLVDPPEPVTWNSGALTSGVHTFPVAVLQSS 62
DB 1 ASTKGPSVPELPAPSSKSTSGTAALGCLVDPPEPVTWNSGALTSGVHTFPVAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKV----- 100
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKKV----- 100
QY 101 -----EPKSCDKTHTCPPCPAPELGCGPSVFLFPKPKDPT 135
DB 121 DTPPPCPKPCPKDPTPPCPKPCPKDPTPPCPAPELGCGPSVFLFPKPKDPT 180
QY 136 LMSIRTPVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 195
DB 181 LMSIRTPVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 240
QY 196 QDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
DB 241 QDWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 300
QY 256 GFVPSDIAVWESNGQPPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHE 315
DB 301 GFVPSDIAVWESNGQPPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHE 360
QY 316 ALHNHYTQKSLSLSPGK 332
DB 361 ALHNHYTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C/Accession: A93906; A92809; A90752; A93132; A02148
R/Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A/Reference number: A93906; MUID:82197621; PMID:6904948
A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:96066056
A/Note: Lys-326 is probably removed posttranslationally
R/Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A/Reference number: A92809; MUID:81007873; PMID:6774012
A/Contents: myeloma protein TIL
A/Accession: A92809
A/Molecule type: protein
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>
A/Note: Trp-156 is at or near the complement-binding site
R/Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A/Title: The amino acid sequences of the three heavy chain constant region domains of a
A/Reference number: A90752; MUID:80001357; PMID:113060
A/Contents: myeloma protein Zie
A/Accession: A90752
A/Molecule type: protein
A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A/Note: This sequence has since been revised
R/Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A/Reference number: A93132; MUID:80114419; PMID:118920
A/Contents: Zie
A/Accession: A93132

A/Molecule type: protein
A/Residues: 238-275 <HOF>
R/Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R/Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A/Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500; PMID:4940472
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R/Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A/Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124; PMID:5782707
A/Contents: annotation; Sa, disulfide bonds
C/Genetics:
A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM1>
F/123-202/Domain: immunoglobulin homology <IM2>
F/123-306/Domain: immunoglobulin homology <IM3>
F/14/Disulfide bonds: interchain (to light chain) #status experimental
F/127-83,140-200,246-304/Disulfide bonds: #status experimental
F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.2%; Score 1604; DB 1; Length 326;
Best Local Similarity 91.2%; Pred. No. 3.9e-105;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 3 ASTKGPSVPELPAPSSKSTSGTAALGCLVDPPEPVTWNSGALTSGVHTFPVAVLQSS 62
DB 1 ASTKGPSVPELPAPSSKSTSGTAALGCLVDPPEPVTWNSGALTSGVHTFPVAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKHTCPCPAPELGG 122
DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTPKVDKVPKSCDKHTCPCPAPELGG 116
QY 123 PSVFLFPKPKDPTLMSIRTPVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182
DB 117 PSVFLFPKPKDPTLMSIRTPVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 176
QY 183 STYRWVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 177 STYRWVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 236
QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 302
DB 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 296
QY 303 QGQNVFSCVWHEALHNHYTQKSLSLSPGK 332
DB 297 QGQNVFSCVWHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999
C/Accession: A90933; A90249; A02150
R/Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A/Title: Nucleotide sequence of a human immunoglobulin C-gamma 4 gene.
A/Reference number: A90933; MUID:83157104; PMID:6299662

Db 177 STYRVSVLPVPIQHDWLNGKEFKCKVNNKDLPAPIITRIISKAKGQTRPQVYTLPPHAE 236
 QY 243 LTKNOVSLCLVKGFPSPDIWESNGQ--PNNYKTTTPVPLDSGSPFLYKSLTVDKS 300
 Db 237 LSRKSVITCLVIGFPPDIDWQNGQPEPEGNRYRTTPQODVGTGYLYSKFSVDKA 296
 QY 301 RWOQGNVFCSCVMHEALHNYHTQKSLSPGK 332
 Db 297 SWOGGIFQCAVMHEALHNYHTQKSLSPGK 328

RESULT 8

S31866
 Ig gamma-1 chain C region - synthetic
 A:Species: synthetic
 A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
 C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
 C:Accession: S31866
 R:Filpula, D.
 submitted to the EMBL Data Library, February 1993
 A:Description: Screening method for protein-protein interactions of cloned gene products.
 A:Reference number: S31866
 A:Accession: S31866
 A:Molecule type: mRNA
 A:Residues: 1-255 <FIL>
 A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069
 C:Keywords: immunoglobulin
 F:1-22/Region: Escherichia coli outer membrane protein A precursor
 F:23-255/Region: human Ig gamma-1 chain C region

Query Match 70.9%; Score 1260; DB 4; Length 255;
 Best Local Similarity 97.5%; Pred. No. 3.6e-81;
 Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 94 TKVDKKEPKSCDKTHTCPCPAPELLGGPSVFLPPPKDPLMISRTPEVTCVVVDVSH 153
 Db 17 TAAQADVESKCDKTHCTCPCPAPELLGGPSVFLPPPKDPLMISRTPEVTCVVVDVSH 76
 QY 154 EPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVQLHQLDNLGKEYCKKYSNKA 213
 Db 77 EPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVQLHQLDNLGKEYCKKYSNKA 136
 QY 214 PAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIWESNGQPE 273
 Db 137 PAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIWESNGQPE 196
 QY 274 NNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSPGK 332
 Db 197 NNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKSLSPGK 255

RESULT 9

I47160
 Ig gamma 2b chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47160
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126
 C:Genetics:
 A:Gene: IgG2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IMM>
 Query Match 70.7%; Score 1257; DB 2; Length 328;
 Best Local Similarity 69.3%; Pred. No. 8e-81;

Matches 230; Conservative 42; Mismatches 54; Indels 6; Gaps 2;
 QY 3 ASTKGPVFLAPLAPSKSTSGTAALGCLVXDYPPPEVTVSWNSGALTSGVHTTFAVLQSS 62
 Db 1 APKTAPLVYFLAPCGRTSGPNVALGCLASSYPPPEVTVTWNSGALTSGVHTTFAVLQPS 60
 QY 63 GLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHTCPCPAPELLGG 122
 Db 61 GLYSLSVTVTPASSLSKSYTCNVNHPATITTKVDKRGVTKTPPCPICACSP----G 116
 QY 123 PSVELFPPKPKDPLMISRTPEVTCVVVDVSHDEPVEVKFNWYVDGVEVHNATKPREEQYN 182
 Db 117 PSVEFPPKPKDPLMISRTPEVTCVVVDVSHDEPVEVKFNWYVDGVEVHNATKPREEQYN 176
 QY 183 STYRVSVLTVQLHQLDNLGKEYCKKYSNKAIPAKETISKAKQPREPOVYTLPPSRDE 242
 Db 177 STYRVSVLPVPIQHDWLNGKEFKCKVNNKDLPAPIITRIISKAKGQTRPQVYTLPPHAE 236
 QY 243 LTKNOVSLCLVKGFPSPDIWESNGQ--PNNYKTTTPVPLDSGSPFLYKSLTVDKS 300
 Db 237 LSRKSVITCLVIGFPPDIDWQNGQPEPEGNRYRTTPQODVGTGYLYSKFSVDKA 296
 QY 301 RWOQGNVFCSCVMHEALHNYHTQKSLSPGK 332
 Db 297 SWOGGIFQCAVMHEALHNYHTQKSLSPGK 328

RESULT 10

PT0207
 Ig gamma chain C region - chimpanzee
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 C:Accession: PT0207
 R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A:Title: Nucleotide sequence of chimpanzee Cc and hinge regions.
 A:Reference number: PT0207; MUID:91287716; PMID:2062315
 A:Accession: PT0207
 A:Molecule type: mRNA
 A:Residues: 1-234 <EHR>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 70.5%; Score 1254; DB 2; Length 234;
 Best Local Similarity 98.7%; Pred. No. 8.5e-81;
 Matches 231; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 92 SNTKVDKKEPKSCDKTHTCPCPAPELLGGPSVFLPPPKDPLMISRTPEVTCVVVDV 151
 Db 1 SNTKVDKKEPKSCDKTHTCPCPAPELLGGPSVFLPPPKDPLMISRTPEVTCVVVDV 60
 QY 152 SHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVQLHQLDNLGKEYCKKYSNK 211
 Db 61 SHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVQLHQLDNLGKEYCKKYSNK 120
 QY 212 ALPAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIWESNGQ 271
 Db 121 ALPAPIETISKAGQPREPOVYTLPPSRDELTKNOVSLCLVKGFPSPDIWESNGQ 180
 QY 272 PENNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKS 325
 Db 181 PENNYKTTTPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNYHTQKS 234

RESULT 11

I47158
 Ig gamma 1 chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47158
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 1 AKTAPSVYPLAPCDRTSGENVALGCLASSYFPEPTVTWNSGALTSGVHTFPAVLQPS 60
 QY 63 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELLGG 122
 DB 61 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELLGG 116
 QY 123 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKENFVVDGVEVHNATKPREQYN 182
 DB 117 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKENFVVDGVEVHNATKPREQYN 176
 QY 183 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSRDE 242
 DB 177 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSRDE 236
 QY 243 LTKNOVSLTCLVKGYPSDIAVEWESNGQ--PENNYKTTTPVLSDDSGSFFLYSKLTVDKS 300
 DB 237 LRSKVTYVCLVIGFYPPDIHVEWKSNGQPEPEGNRYTRTPQDDVGTFFLYSKLAVDKA 296
 QY 301 RMOQGNFVSCSVNHEALHNHYTQKSLSLSPGK 332
 DB 297 RWDHGETFECAVWHEALHNHYTQKSLSLSPGK 328
 RESULT 14
 G2GP
 Ig gamma-2 chain C region - guinea pig
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999
 C/Accession: A94553; A90352; A90359; A90384; A90385; A02151
 R./Frischmann, T.M.
 submitted to the Atlas, April 1975
 A/Reference number: A94553
 A/Accession: A94553
 A/Molecule type: protein
 A/Residues: 1-3 <TRI>
 R./Srinivasan, B.K.; Hussain, Q.Z.; Cebra, J.J.
 Biochemistry 10, 18-25, 1971
 A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
 A/Reference number: A90352; MUID:71058471; PMID:5538606
 A/Accession: A90352
 A/Molecule type: protein
 A/Residues: 4-68 <BIR>
 R./Turner, K.J.; Cebra, J.J.
 Biochemistry 10, 9-17, 1971
 A/Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
 A/Reference number: A90359; MUID:71058486; PMID:5538616
 A/Accession: A90359
 A/Molecule type: protein
 A/Residues: 69-133/312-329 <TUR>
 R./Ritcey, D.E.; Cebra, J.J.
 Biochemistry 13, 4796-4803, 1974
 A/Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
 A/Reference number: A90384; MUID:75036072; PMID:4429665
 A/Accession: A90384
 A/Molecule type: protein
 A/Residues: 134-226 <TRA>
 R./Frischmann, T.M.; Cebra, J.J.
 Biochemistry 13, 4804-4811, 1974
 A/Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
 A/Reference number: A90385; MUID:75036073; PMID:4609467
 A/Accession: A90385
 A/Molecule type: protein
 A/Residues: 227-311 <TR2>
 R./Oliveira, B.; Lamm, M.E.
 Biochemistry 10, 26-31, 1971
 A/Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
 A/Reference number: A90354; MUID:71058474; PMID:4922544
 A/Contents: annotation: disulfide bonds
 A/Note: Cys-16 is involved in a heavy-light chain bond
 A/Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds

C/Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) and two identical heavy (H) chains. In some cases, such as IgA and IgM, the subunits associate into a chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a chain disulfide bonds.
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F/21-81/Domain: immunoglobulin homology <IM1>
 F/135-204/Domain: immunoglobulin homology <IM2>
 F/241-310/Domain: immunoglobulin homology <IM3>
 F/28-79/Disulfide bonds: #status experimental
 F/142-202/Disulfide bonds: #status experimental
 F/178/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F/248-308/Disulfide bonds: #status experimental

Query Match 68.2%; Score 1212.5; DB 1; Length 329;
 Best Local Similarity 70.3%; Pred. No. 1.1e-77;
 Matches 234; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 2 ARTAPSVFPLAASCVDTSNMVTLGCLVKGYFPEPTVTKNSGALTSGVHTFPAVLQ-S 60
 QY 63 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELL 120
 DB 61 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELL 116
 QY 121 GGPVSFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180
 DB 117 GGPVSFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 176
 QY 181 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSR 240
 DB 177 YNTYTRVSVLTVLHODWLNKGYCKVSNKALPAPIETIKTSKAKQPREPQVYTLPPSR 236
 QY 241 DELTKNOVSLTCLVKGYPSDIAVEWESNGQ--PENNYKTTTPVLSDDSGSFFLYSKLTVD 298
 DB 237 DELSKSKSVTCLINFPADTHVENSNRVPSKEYKNTPEIDAGSGVFLYSLTVD 296
 QY 299 KSRWQGNFVSCSVNHEALHNHYTQKSLSLSPG 331
 DB 297 KSAWDQGVYTCVSNHEALHNHYTQKSLSLSPG 329

RESULT 15
 S31459
 Ig gamma-1 chain - sheep (fragment)
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C/Accession: S31459
 R./Patri, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A/Reference number: S31459
 A/Accession: S31459
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-472 <PAT>
 A/Cross-references: EMBL:X59797
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: immunoglobulin
 F/277-346/Domain: immunoglobulin homology <IM>

Query Match 67.5%; Score 1199.5; DB 2; Length 472;
 Best Local Similarity 67.5%; Pred. No. 1.3e-76;
 Matches 224; Conservative 38; Mismatches 67; Indels 3; Gaps 2;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 142 ASTTTPKVPYPLTSCCGDTSSISVTLGCLVSSVPEPTVTSWNSGALTSGVHTFPAVLQSS 201
 QY 63 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELLGG 122
 DB 202 GLYSLSVVTVPSLSGLTQTYICNVNHPKSNKVDKVEPKSCDKTH--TCPPCPAPELLGG 260
 QY 123 PSVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 182

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 14.4378 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFATKGPSVFLAPSSKST.....MHEALHNHYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	99.4	330	1 GCI_HUMAN	P01857 homo sapien
2	1604	90.2	326	1 GCI_HUMAN	P01859 homo sapien
3	1590.5	89.5	327	1 GCI_HUMAN	P01861 homo sapien
4	1230.5	69.2	323	1 GC_RABIT	P01870 oryctolagus
5	1212.5	68.2	329	1 GC2_CAVPO	P01862 cavia porce
6	1156	65.0	290	1 GCI_HUMAN	P01860 homo sapien
7	1152	64.8	326	1 GCI_RAT	P02759 rattus norv
8	1146.5	64.5	333	1 GCB_RAT	P20761 rattus norv
9	1142	64.2	324	1 GCI_MOUSE	P01868 mus musculu
10	1141	64.2	329	1 GCI_MOUSE	P22436 mus musculu
11	1137	63.9	393	1 GCI_MOUSE	P01869 mus musculu
12	1130	63.6	398	1 GCI_MOUSE	P03987 mus musculu
13	1126	63.3	330	1 GCAA_MOUSE	P01863 mus musculu
14	1123.5	63.2	335	1 GCB_MOUSE	P01864 mus musculu
15	1121	63.0	399	1 GCB_MOUSE	P01865 mus musculu
16	1118.5	62.9	329	1 GCC_RAT	P02762 rattus norv
17	1112	62.5	322	1 GCA_RAT	P20760 rattus norv
18	1087	61.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1082	60.9	405	1 GCB_MOUSE	P01867 mus musculu
20	492	27.7	428	1 EPC_HUMAN	P01854 homo sapien
21	483.5	27.2	429	1 EPC_RAT	P01855 rattus norv
22	468	26.3	421	1 EPC_MOUSE	P06336 mus musculu
23	444	25.0	454	1 MUC_HUMAN	P01871 homo sapien
24	439	24.7	458	1 MUC_RABIT	P03988 oryctolagus
25	429.5	24.2	455	1 MUC_MOUSE	P01872 mus musculu
26	429	24.1	479	1 MUC_RABIT	P04221 oryctolagus
27	422	23.7	457	1 MUC_SUNMU	P20768 suncus muri
28	419.5	23.6	476	1 MUC_MOUSE	P01873 mus musculu
29	417	23.5	450	1 MUC_CANFA	P01874 canis famil
30	415.5	23.4	454	1 MUC_MESAU	P06337 mesocricetu
31	402	22.6	391	1 MUCB_HUMAN	P04220 homo sapien
32	395	22.2	438	1 HVCS_HETFR	P23087 heterodontu
33	386	21.7	461	1 HVCM_HETFR	P23088 heterodontu

ALIGNMENTS

RESULT 1

ID	GCI_HUMAN	STANDARD	PRT	330 AA
AC	P01857; 1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	IG gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Maxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	Biochemistry 9:3161-3170(1970).			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	Biochemistry 9:3171-3181(1970).			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070289; PubMed=828475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RL	peptides and discussion of the complete structure."			
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RT	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

34	385.5	21.7	438	1	HVC2_HETFR	P23085 heterodontu
35	384.5	21.6	353	1	ALCI_HUMAN	P01876 homo sapien
36	381.5	21.5	353	1	ALCI_GORGO	P20758 gorilla gor
37	380	21.4	370	1	HVC1_HETFR	P23084 heterodontu
38	379	21.3	340	1	ALC2_HUMAN	P01877 homo sapien
39	363	20.4	393	1	HVC3_HETFR	P23086 heterodontu
40	348	19.6	344	1	ALC_MOUSE	P01878 mus musculu
41	329	18.5	446	1	MUC_CHICK	P01875 gallus gall
42	320	18.0	299	1	ALC_RABIT	P01879 oryctolagus
43	290.5	16.3	481	1	MUCM ICTPU	P23735 ictalurus p
44	223.5	12.6	383	1	DTC_HUMAN	P01880 homo sapien
45	194.5	10.9	513	1	SHSI_MOUSE	P97797 m protein-t

QY 303 QCGNVFSCVMEALHNYHTQKSLSPCK 332
 DB 301 QCGNVFSCVMEALHNYHTQKSLSPCK 330

RESULT 2
 GC2_HUMAN
 ID GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE IG gamma-2 chain C region.
 GN IGHG2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RX TISSUE=Fetal liver;
 RC MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 RT evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RT genes";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IGH2 heavy chain: genetic,
 RT evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RT domains of a human IGH2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RT immunoglobulin gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RT immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 DR EMBL; J00230; AAB59393.1; -.
 DR PIR; A93906; G2HU.
 DR HSP; P01857; LFC1.
 DR Genew; HGNC:5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00407; IGC1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 1 98
 FT DOMAIN 99 110 CH1.
 FT DOMAIN 111 219 HINGE.
 FT DOMAIN 220 326 CH2.
 FT DISULFID 14 14 CH3.
 FT DISULFID 27 83 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109
 FT CONFLICT 326 AA; 35884 MW; 83108786879C CRC64;
 SQ SEQUENCE

Query Match 90.2%; Score 1604; DB 1; Length 326;
 Best Local Similarity 91.2%; Pred. No. 1.2e-113;
 Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKVKPEKSCDKTHCTCPCPAPELGG 122
 DB 61 GLYSLSSVTVTPSSNFGTQTYTCNVNKPSTKVDKTKVERKCCVE---CPCPAPP-VAG 116
 QY 123 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGVGVHNAKTKPREOYN 182
 DB 117 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGVGVHNAKTKPREOYN 176

QY 183 STYRVSVLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 242
 DB 177 STFRVSVLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 236
 QY 243 LTKQVSLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 302
 DB 237 MTKQVSLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 296
 QY 303 QQGNVFCSCVNHVHEALHNHYTKSLSPGK 332
 DB 297 QQGNVFCSCVNHVHEALHNHYTKSLSPGK 326

RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
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 CC EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A90933; GAHU.
 DR PDB; 1ADQ; 16-SEP-98.
 DR GenBank; HGNC:5528; IGHG4.
 DR MIM; 147130;
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding activity; TAS.
 DR GO; GO:0006955; F:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003106; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGH1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 220 CH2.
 FT DOMAIN 221 327 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 141 201
 FT DISULFID 247 305
 SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811BF208E7A CRC64;
 Query Match 89.5%; Score 1590.5; DB 1; Length 327;
 Best Local Similarity 90.9%; Pred. No. 1.2e-112;
 Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSSVTVPPSSSLGTQTYICNNHKPSNTKVDKVEPKSKDKTHTCPCPAPELGG 122
 DB 61 GLYSLSSVTVPPSSSLGTQTYICNVHDKPSNTKVDKVESK--YGPSPSCPAPPELGG 117
 QY 123 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDDEVKFNMYVDGVEVHNNAKTKRESQYN 182
 DB 118 PSVFLFPPPKDITLMISRTPEVTCVVDVSHEDDEVKFNMYVDGVEVHNNAKTKRESQFN 177
 QY 193 STYRVSVLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 242
 DB 178 STYRVSVLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 237
 QY 243 LTKQVSLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 302
 DB 238 MTKQVSLTCLVKGFPYSDIAVEWESGQPNENYKTTTPVLDSDGFFFLYSLKLTVDKSRW 297
 QY 303 QQGNVFCSCVNHVHEALHNHYTKSLSPGK 332
 DB 298 QQGNVFCSCVNHVHEALHNHYTKSLSPGK 327

RESULT 4
 GC RABIT
 ID GC RABIT STANDARD; PRT; 323 AA.
 AC P01870;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84030930; PubMed=6313520;
 RA Bernstein K.E., Alexander C.B., Mage R.G.;
 RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
 F-I haplotype.";
 RL Immunogenetics 18:387-397(1983).
 RN [2]
 RP SEQUENCE OF 1-128.
 RX MEDLINE=76135469; PubMed=1243651;
 RA Pratt D.M., Mole L.E.;
 RT "Sequence studies on the constant region of the Fd sections of rabbit
 immunoglobulin G of different allotype.";
 RL Biochem. J. 151:337-349(1975).
 RN [3]
 RP SEQUENCE OF 88-266 FROM N.A.
 RX MEDLINE=83299917; PubMed=6193512;
 RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
 RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
 heavy chain and identification of two genomic C gamma genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 RN [4]
 RP SEQUENCE OF 132-161.
 RX MEDLINE=70110015; PubMed=5461106;
 RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
 RT "Sequence studies of the Fd section of the heavy chain of rabbit
 immunoglobulin G.";

RL Biochem. J. 116:249-259 (1970).
 RN [5]
 RP SEQUENCE OF 129-131 AND 155-322.
 RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
 RL (in) Kallander J. (eds.);
 RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
 RL Stockholm (1967).
 CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
 CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
 CC MARKERS AND REF.5 THE E15 MARKER.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M16426; AAA31289.1; -;
 DR PIR: A91749; GHRB.
 DR HSSP: P01857; 1FC1.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00407; Igc1; 2.
 DR PROSITE: PS00835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region; Repeat.
 DR NON TER 1
 FT DOMAIN 1 96
 FT DOVAIN 114 213
 FT DOVAIN 222 318
 FT VARIANT 104 104
 FT VARIANT 185 185
 FT CONFLICT 48 48
 FT CONFLICT 71 71
 FT CONFLICT 144 144
 FT CONFLICT 173 173
 FT CONFLICT 187 187
 FT CONFLICT 201 201
 FT CONFLICT 218 218
 FT CONFLICT 233 233
 FT CONFLICT 246 246
 FT CONFLICT 256 256
 FT CONFLICT 260 260
 FT CONFLICT 266 266
 FT CONFLICT 280 280
 FT CONFLICT 284 284
 SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;
 Query Match 69.2%; Score 1230.5; DB 1; Length 323;
 Best Local Similarity 70.0%; Pred. No. 1.5e-85;
 Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;
 QY 6 KGPSVFLAPSKSTSGTAAALGCLVDFPFPVTVSWNSGALTSVGHVTPAVLQSSGLY 65
 DB 4 KAPSVFLAPCCGTPSPSTVTLGCLVKGYPFPVTVTWSGTLTNGVTFPFSVRQSSGLY 63
 QY 66 SLSSVTVFPSSSLGTQYICNVNHPKNTKVKKPEKSCDKTHTCPCPAPELLGGPSV 125
 DB 64 SLSSVTVFTSS---QPVTCNVAPATNTKVDVTAPSTCSK---FTCPPPPELLGGPSV 116
 QY 126 FLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKPKPEQVNSTY 185
 DB 117 FIFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKPKPEQVNSTY 176
 QY 186 RVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPVYTLPPSRDELTK 245
 DB 177 RVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPVYTLPPSRDELTK 236

QY 246 NOVSLTCLYKGFPSDIAVWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQG 305
 DB 237 RSVSLTCLYKGFPSDIAVWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQG 296
 QY 306 NVFSSVWHEALHNYTKSLSPCK 332
 DB 297 DVFTCSVWHEALHNYTKSLSPCK 323
 RESULT 5
 ID GC2 CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig gamma-2 chain C region.
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birshstein B.K.; Huseain Q.Z.; Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cysteine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J.; Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E.; Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M.; Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE=71058474; PubMed=4922544;
 RA Oliveira B.; Lamm M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RL Biochemistry 10:26-31(1971).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 CC 13 INBRED GUINEA PIGS.
 CC PIR: A94553; G2GP.
 DR HSSP: P01842; 7FAB.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig; 2.
 DR SMART: SM00407; Igc1; 2.
 DR PROSITE: PS00835; IG-LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

```
FT NON TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 68.2%; Score 1212.5; DB 1; Length 329;
Best Local Similarity 70.3%; Pred. No. 3.5e-84;
Matches 234; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 3 ASTKGPSVFLPAPSSKSTGGTAAALCGLVKDYFPEPTVWNSGALTSGVHTFPVAVLOSS 62
DB 2 ARTAPSVFLPAAASCVDTSGMMTGLCLVKGYFPEPTVWNSGALTSGVHTFPVAVLQ-S 60
QY 63 GLYSLSGVTVPRSSSLGTQYICNVNHNKSNKNTVDKKVPEKSCDKTH--TCPPCAPPELL 120
DB 61 GLYSLSMTVTPSSQKAT-----CNVAHPASSSTKVDKTFPIPTPZBPCTCKPCPPENL 116
QY 121 GGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVFNFNVDGVEVHNNAKTKPREEQ 180
DB 117 GGPSVFIFFPKPKDTLMISLTPRTVCVVDVSDPEVQFTFVDNKPVGNAETKPRVEQ 176
QY 181 YNSTYRVSVLTVLHQWLNGKKEYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 240
DB 177 YNTTFRVESVLPVTHQDNLGKGEFKCKVYKNAKALPAPIETISKAKGPMPPVYTLPPSR 236
QY 241 DELTKQVSLTCLVKGYFSDIAVESNGQP--ENNYKTPPVLDSDGSFELYSKLTVD 298
DB 237 DELSKKSVSTCLLIINFFPADIHVENASNPVSEKEYKNTPIEDADGSFELYSKLTVD 296
QY 299 KSRWQQNVFSCVMHEALHNHYTKSLSPG 331
DB 297 KSAWDQGVTVTCVMHEALHNHYTKAISRSPG 329

RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RA MEDLINE=81021549; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein WIS.";
RN Biochemistry 19:4304-4308(1980).
RP REVISIONS TO 12-97 (PROTEIN WIS).
RA MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.";
RN J. Biol. Chem. 252:883-889(1977).
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RA MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Rodel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RL Structure of the FC fragment of immunoglobulin G3.";
RT
```

```
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=92247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF.2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CH1 REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
CC -----
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CC -----
DR EMBL; J00231; AAAS2805.1; ALT_SEQ.
DR HSSP; P01857; 1FC1.
DR Genew; HGNC:5527; IGHG3.
DR MIM; 147120; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; P:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Immunoglobulin carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 24 24 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 27 27 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 33 33 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 39 39 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 42 42 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 48 48 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 54 54 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 57 57 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 63 63 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 69 69 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT DISULFID 72 72 INTERCHAIN (WITH HEAVY CHAIN DIMER).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .).
FT MOD_RES 230 290 REMOVED POST-TRANSLATIONALLY.
```

FT VARIANT 126 127 QV -> EB (IN ZUC).
 FT VARIANT 134 134 /FTID=VAR_003890.
 FT VARIANT 134 134 F -> L (IN OMM).
 FT VARIANT 139 139 /FTID=VAR_003891.
 FT VARIANT 139 139 F -> Y (IN OMM).
 FT VARIANT 182 182 /FTID=VAR_003892.
 FT VARIANT 182 182 T -> A (IN OMM).
 FT VARIANT 227 227 /FTID=VAR_003893.
 FT VARIANT 227 227 S -> N (IN OMM).
 FT VARIANT 227 227 /FTID=VAR_003894.
 FT VARIANT 227 227 MISSING (IN ZUC).
 FT VARIANT 279 279 /FTID=VAR_003895.
 FT VARIANT 279 279 F -> Y (IN OMM).
 FT VARIANT 279 279 /FTID=VAR_003896.
 SQ SEQUENCE 290 AA; 32331 MW; E69CB957052F46 CRC64;

Query Match 65.0%; Score 1156; DB 1; Length 290;
 Best Local Similarity 90.5%; Pred. No. 5.3e-80;
 Matches 210; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 101 EPKSCDTHCTPCPCAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 160
 DB 59 EPKSCDTHCTPCPCAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 118
 QY 161 NWYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 220
 DB 119 KWIYDGVGVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 178
 QY 221 ISKAKQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 280
 DB 179 ISKTKGQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 238
 QY 281 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 332
 DB 239 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 290

RESULT 7
 GC1_RAT ID GC1_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."
 RL Gene 74:473-482(1988).
 DR PIR; PS0017; PS0017.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 64.8%; Score 1152; DB 1; Length 326;
 Best Local Similarity 63.1%; Pred. No. 1.2e-79;
 Matches 210; Conservative 53; Mismatches 60; Indels 10; Gaps 4;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPPBPVTVSNKSGALTSGVHTFPAVLQSS 62
 DB 1 AETAPSVPLAPAGTALKNSMTLGLCLVKGFPPBPVTVSNKSGALTSGVHTFPAVLQ-S 59
 QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVKEPKSCDKHTHTCPPCPAPPELLGG 122
 DB 60 GLYTLTSSVTVPPSSVPSQTVCNVAHPASSTKVDKIVPRNCG--GDCKPC---ICTG 113
 QY 123 ---PSVLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 179
 DB 114 SEVSSVFIPPPKKDTLITLPKVTCTVVDVLSQDDPEVHFVDFVDDVEVHTAQRPEE 173
 QY 180 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 239
 DB 174 QNSIFRSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTIKSPGRTQVPHVYTMSP 233
 QY 240 RELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 299
 DB 234 KEEMTQNEVSIICMKVGFYPPDIYVEWQNGQPQENYKNTPTMTDGTGSIYFLSKLVK 293
 QY 300 SRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 332
 DB 294 EXWQGNITFCSVLHLEGLHNHHTKSLSHSPGK 326

RESULT 8
 GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."
 RL Gene 74:473-482(1988).
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
 DR PIR; PS0018; PS0018.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 1 96 IG-LIKE 1.
 FT DOMAIN 124 223 IG-LIKE 2.
 FT DOMAIN 232 328 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

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FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match
Best Local Similarity 64.58; Score 1146.5; DB 1; Length 333;
Matches 215; Conservative 44; Mismatches 68; Indels 9; Gaps 3;

Qy 3 ASTKGSVFLPAPSSKSTSGTAAALGCLVKDYPEPEPTVWNSGALTSVGHVFFPAVLQSS 62
Db 1 AQTAPSVYFLAPGCGDTSTSTVTLGCLVKGYPEPEPTVWNSGALSSDVHFFPAVLQ-S 59

Qy 63 GLYSLSVTVVPSSISGTQYICNVHKSNTKVDKKVPKS-----CDKTHTCPCPA 116
Db 60 GLYLTSSVT--SSTVPSQVTCNVAPASSTKVDKVERNGRGIGHKCTCPTCHKCPV 117

Qy 117 PELLGGSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 176
Db 118 PELLGGSVFLFPKPKDILLISQNAKVCVVVDVSEEPDVFQSFVNNVEVHTAQTP 177

Qy 177 REQYNSTYRVSVLVTLVHODWLNKGEYCKVSKALPAPIETKISKAKGQPREPQVYTL 236
Db 178 REQYNSTYRVSVLVTLVHODWLNKGEYCKVSKALPAPIETKISKAKGQPREPQVYVM 237

Qy 237 PPRKDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTTPVLDSDGSFFELYSLK 296
Db 238 GPTEQLTEGTVSLTCLTSLGFLNDLGVENTSGHIEKRYKNTPEVNDSDGSFFMYSKLN 297

Qy 297 VDKSRWQGNVFCVSNVHEALHNHYTQKSLSLSPGK 332
Db 298 VERSRWDSRAPFVCSVYVHEGLNHNHYEKSISRPPGK 333

RESULT 9
CCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.,
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=8022559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242286; PubMed=98524;
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RA Adetudbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
RT murine myeloma gammal chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=7300889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; V00793; CAA24172.1; -
CC EMBL; V00793; CAA24173.1; -
CC EMBL; V00793; CAA24174.1; -
CC EMBL; V00793; CAA24175.1; -
CC EMBL; V00795; CAA24176.1; -
CC PIR; A02159; GIMS.
CC PDB; 1LGC; 03-JUN-95.
CC GlycoSuiteDB; P01868; -
CC MGD; MGI:96446; Igh-4.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SMC0407; Igc1; 2.
CC PROSITE; PS50835; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; 3D-structure.
FT NON TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT FTIG=CAR_000055.
FT DISULFID 244 302
FT MOD RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match
Best Local Similarity 64.28; Score 1142; DB 1; Length 324;
Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

Qy 3 ASTKGSVFLPAPSSKSTSGTAAALGCLVKDYPEPEPTVWNSGALTSVGHVFFPAVLQSS 62
Db 1 AKTTPSVYFLAPGCGDTSTSTVTLGCLVKGYPEPEPTVWNSGALSSDVHFFPAVLQSD 60

Qy 63 GLYSLSVTVVPSSISLGTQYICNVNHPKNTKVDKVPKSCDKTHTCPP--CPAPELL 120
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or send an email to license@isb-sib.ch)
-----
EMBL; V00793; CAA24172.1; -
EMBL; V00793; CAA24173.1; -
EMBL; V00793; CAA24174.1; -
PIR; B02159; GIMSM.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1AB6; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1F11; 06-FEB-01.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1K25; 24-JUL-02.
DR PDB; 1K29; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane; 3D-structure.
FT NON_TER 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4C688343B7A1CE27 CRC64;

Query Match 63.9%; Score 1137; DB 1; Length 393;
Best Local Similarity 61.9%; Pred. No. 2.1e-78;
Matches 205; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

QY 3 ASTKGSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 AKTTPSVPLAPGSAAGNSMVTGLCLVKGYFPEPVTVSWNSGSLSSGVHTFPAVLQSD 60
QY 63 GLYSLSSVTVFSSSLGCTQYICNVNHPKSTKVKVKPEKSCDKTHTCPP--CPAPELL 120
DB 61 -LYTLSSVTVFSSPRSETVCNVAHPASSITKDKIVPRDGG---CKPCICTVPEV- 114
QY 121 GGSVFLFPKPKDMLMISRTVEVTVVDVSHEDPEVKFNKYDGVGVHNAKTKPREQ 180
DB 115 --SSVFIFFPKPKDVLITLTFRKTVCCVVVDISKDDPEVQFSFVDDVDEVHTAQTQPREQ 172
QY 181 YNSTYRWVSVLTVHODWLNKGEYKCKVSNKALPAPIETIKAKGQREPOVYTLPPSR 240
DB 173 FNSTFRSVELPIHQDNLNGKFKCRVNSAFPAPIETIKTKGRKAPQVITIPPK 232
QY 241 DELTKNQVSLTCLVKGYFSDIAVEWESNGQDENNYKTPFPVLDSDGSGFFLYSKLTVDKS 300
DB 233 EQMAKDKVSLTCLMIDFFEDITVEWQNGQPAENYKNTQIPMTNGSYFVYSKLVNQS 292
QY 301 RWQGNVFSVSNHEALHNHYTQKSLSLSPG 331

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293 NWEAGNTFTCSVLVLEGLHNHHHTKSLSHSPG 323
-----
Db 293 NWEAGNTFTCSVLVLEGLHNHHHTKSLSHSPG 323
-----
RESULT 12
GC3M MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
[2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
-----
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EMBL; J00451; AAB59655.1; -
EMBL; V01526; CAA24767.1; ALT_SEQ.
PIR; A02156; GIMSM.
HSP; P01857; IFC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 63.6%; Score 1130; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 7.2e-78;
Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 4 STKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLTQSSG 63
DB 1 TTTAPSVPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLTQSSG 59

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QY 64 LYSLSVTVVPSSSLGTQYICNVNKPNTKVDKVKPKSCDKTHTCP--PCPAPELLG 121
Db 60 FYLSLSLVTVPSSTWPSQTVICNVNHPASKEHLIKIEPR-IPKSTPPGSCPPGNILG 118
QY 122 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQY 181
Db 119 GPSVFIFPKPKDMLISLTPKVTCTVVDVSEDDPDVHVSWFVDNKEVHTANTQPREAQY 178
QY 182 NSYTRVSVTLVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRD 241
Db 179 NSTFRVVSALPIQHQMWSGKPKCKVNNKALPAPIERTISKPKGSAQTPOVYITLPPPRE 238
QY 242 ELTKNQVSLTCLVKGYFSPSDIAVEWESNGOPENNYKTTTPVLDSDGSFELYSLKLTVDKSR 301
Db 239 QMSKKVSLTCLVNTFSEALSVEWERNGELEQDYKNTFPILDSGTYFLYSLKLTVDTS 298
QY 302 WQGNVPSGVMHEALHNHYTQKSLSLSP 330
Db 299 WLOGEIFTCSVWHEALHNHHTKQNLGRSP 327

RESULT 13
GCAB MOUSE STANDARD; PRT; 330 AA.
ID GCAB MOUSE AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Skorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RL Balb/c gamma 2a heavy chain messenger RNA.";
RN Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RL and evolution of heavy chain genes: further evidence for intervening
RN sequence-mediated domain transfer.";
RN Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=8123894; PubMed=6787604;
RA Oillo R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RL suggests that exons can be exchanged between genes in a multigenic
RN family.";
RN Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RL immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RN for the evolution of immunoglobulin structure and function.";
RN Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma C2a
RL immunoglobulin. Identification of the disulfide bridges.";
RN Eur. J. Biochem. 30:452-462(1972).
CC 1- SIMILARITY: Contains 3 immunoglobulin-like domains.
-----

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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; V00798; CAA24178.1; --
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 63.3%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. No. 1.e-77;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGPSVFPLAPSSKSTGTGAAALGLVKDYDPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 AKTTAPSVYPLAPVCGDTTGTSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60
QY 63 GLYSSSVTVVPSSSLGTQYICNVNKPNTKVDKVKPKSCDKTHTCP--CPAPELL 120
Db 61 -LYTSLSSVTVSTWPSQITCNVAHPASSTKYDKKIEPRG-PTIKPCKPKCPAPNLL 118
QY 121 GPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNATKPREEQ 180
Db 119 GPSVFIFPKPKDMLISLTPKVTCTVVDVSEDDPDVHVSWFVDNKEVHTANTQTHRED 178
QY 181 YNSTYRVSVTLVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 240
Db 179 YNSTLRVVSALPIQHQMWSGKPKCKVNNKALPAPIERTISKPKGSAQTPOVYITLPPPE 238
QY 241 DELTKNQVSLTCLVKGYFSPSDIAVEWESNGOPENNYKTTTPVLDSDGSFELYSLKLTVDKS 300
Db 239 EEMTKQVTLTCMVTDPMEDIVVEWTNNGKTELNYKNTPEVLDSDGSFYFMSKLKRVKK 298
QY 301 RWQGNVPSGVMHEALHNHYTQKSLSLSPGK 332
Db 299 NWVERNSYSGSVWHEGLNHNHHTKSFSTRPGK 330

RESULT 14
GCAB MOUSE STANDARD; PRT; 335 AA.
ID GCAB MOUSE AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
-----

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 59.441 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778
Sequence: 1 EFASIKGPSVFLAPSSKST.....MHEALHNHYTKSLSPCK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	99.4	471	Q8TC77	Q8TC77 homo sapien
2	1626.5	91.5	521	Q8N4Y9	Q8N4Y9 homo sapien
3	1615.5	90.9	509	Q8NF17	Q8NF17 homo sapien
4	1590.5	89.5	473	Q8TC63	Q8TC63 homo sapien
5	1266.5	71.2	337	Q9SM34	Q9SM34 equus caball
6	1264	71.1	701	Q9SPQ8	Q9SPQ8 homo sapien
7	1161	65.3	469	Q9R3V9	Q9R3V9 mus musculus
8	1155	65.0	463	Q9RLC4	Q9RLC4 mus musculus
9	1151	64.7	437	Q9RIA4	Q9RIA4 mus musculus
10	1137.5	64.0	473	Q9D8L4	Q9D8L4 mus musculus
11	1122	63.1	468	Q9SL31	Q9SL31 mus musculus
12	1122	63.1	473	Q9SL25	Q9SL25 mus musculus
13	1088	61.2	473	Q9IZ05	Q9IZ05 mus musculus
14	1088	61.2	474	Q9R3H6	Q9R3H6 mus musculus
15	444.5	25.0	597	Q9BU10	Q9BU10 homo sapien
16	444.5	25.0	597	Q9BQ88	Q9BQ88 homo sapien

17	444.5	25.0	597	4	Q96BB9	Q96BB9 homo sapien
18	436.5	24.6	278	11	Q921K1	Q921K1 mus musculus
19	434.5	24.4	588	4	Q8WUX4	Q8WUX4 homo sapien
20	434.5	24.4	613	4	Q96EY0	Q96EY0 homo sapien
21	434.5	24.4	613	4	Q8WUK1	Q8WUK1 homo sapien
22	434.5	24.4	614	4	Q96GA6	Q96GA6 homo sapien
23	434.5	24.4	618	4	Q96AA6	Q96AA6 homo sapien
24	434.5	23.6	613	11	Q8VCX7	Q8VCX7 mus musculus
25	398	22.4	375	4	Q9BSZ1	Q9BSZ1 homo sapien
26	384.5	21.6	384	4	Q9UP60	Q9UP60 homo sapien
27	384.5	21.6	493	4	Q8NCL6	Q8NCL6 homo sapien
28	384.5	21.6	494	4	Q96K68	Q96K68 homo sapien
29	384.5	21.5	495	4	Q96KX8	Q96KX8 homo sapien
30	381.5	21.5	495	4	Q96DK0	Q96DK0 homo sapien
31	381.5	21.5	499	4	Q8NSK4	Q8NSK4 homo sapien
32	379.5	21.3	497	4	Q8WY24	Q8WY24 homo sapien
33	379.5	21.3	500	4	Q9BRV0	Q9BRV0 homo sapien
34	379	21.3	416	4	Q9NPP6	Q9NPP6 homo sapien
35	370	20.8	486	11	Q91Z07	Q91Z07 mus musculus
36	370	20.8	487	11	Q99KA4	Q99KA4 mus musculus
37	370	20.8	584	13	Q90544	Q90544 ginglymosto
38	369	20.8	426	11	Q9DCD9	Q9DCD9 mus musculus
39	356.5	20.1	481	11	Q91WT3	Q91WT3 mus musculus
40	356.5	20.1	481	11	Q91WT1	Q91WT1 mus musculus
41	356.5	20.1	482	11	Q91X92	Q91X92 mus musculus
42	356.5	20.1	482	11	Q8K172	Q8K172 mus musculus
43	356.5	20.1	484	11	Q8VEA0	Q8VEA0 mus musculus
44	356.5	20.1	488	11	Q91WR1	Q91WR1 mus musculus
45	356.5	20.1	488	11	Q8K0F2	Q8K0F2 mus musculus

ALIGNMENTS

RESULT 1

Q8TC77 PRELIMINARY; PRT; 471 AA.
ID Q8TC77;
AC Q8TC77;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Splice;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 99.4%; Score 1767; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-152;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	3	ASTKGPSVFLAPSSKSTGGTAAAGLVKDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 62
Db	142	ASTKGPSVFLAPSSKSTGGTAAAGLVKDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 201
Oy	63	GLYSLSSVWTVPPSSLSGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 122
Db	202	GLYSLSSVWTVPPSSLSGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 261

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QY 123 PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
Db 262 PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 321
QY 183 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 322 STYRVSVLTVLHODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 381
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
Db 382 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 441
QY 303 QCGNVSFCSVMHEALHNHYTQKSLSLSPGK 332
Db 442 QCGNVSFCSVMHEALHNHYTQKSLSLSPGK 471

RESULT 2
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein_521.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 91.5%; Score 1626.5; DB 4; Length 521;
Best Local Similarity 81.7%; Pred. No. 28-139;
Matches 308; Conservative 11; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 62
Db 145 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 204
QY 63 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
Db 205 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
QY 101 -----EPKSCDKHTCTPCPAPPELLGGPSVFLFPPPKD 264
Db 265 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPPELLGGPSVFLFPPPKD 324
QY 136 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVLH 195
Db 325 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVLH 384
QY 196 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
Db 385 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 444
QY 256 GFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 315
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Db 445 GFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 504
QY 316 ALHNHYTQKSLSLSPGK 332
Db 505 ALHNHYTQKSLSLSPGK 521

RESULT 3
Q8NF17 PRELIMINARY; PRT; 509 AA.
AC Q8NF17
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE FLJ00385 protein (Fragment).
GN FLJ00385.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohata O.;
RL "The nucleotide sequence of a long cDNA clone isolated from human
RT spleen."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON TER 1
SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 90.9%; Score 1615.5; DB 4; Length 509;
Best Local Similarity 81.6%; Pred. No. 1.9e-138;
Matches 306; Conservative 11; Mismatches 11; Indels 47; Gaps 1;

QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 62
Db 64 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSQVHTFPAVLQSS 123
QY 63 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
Db 124 GLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV----- 100
QY 101 -----EPKSCDKHTCTPCPAPPELLGGPSVFLFPPPKD 135
Db 184 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPPELLGGPSVFLFPPPKD 243
QY 136 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVLH 195
Db 244 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNSTYRVSVLTVLH 303
QY 196 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
Db 304 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 363
QY 256 GFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 315
Db 364 GFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 423
QY 316 ALHNHYTQKSLSLSP 330
Db 424 ALHNHYTQKSLSLSP 438

RESULT 4
```

```
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 89.5%; Score 1590.5; DB 4; Length 473;
Best Local Similarity 90.9%; Pred. No. 3.2e-136;
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSVNSGALTSGVHTFPAVLQSS 62
DB 147 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSVNSGALTSGVHTFPAVLQSS 206

QY 63 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 122
DB 207 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 122

QY 123 PSVFLPFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKPREEQYN 182
DB 264 PSVFLPFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKPREEQYN 323

QY 183 STYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 324 STYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 383

QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
DB 384 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 443

QY 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
DB 444 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473

RESULT 5
Q95M34
ID Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
GN IGHCL1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199; 105-119 (1998).
DR EMBL; AJ300675; CAC44624.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON_TER
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 71.2%; Score 1266.5; DB 6; Length 337;
Best Local Similarity 69.2%; Pred. No. 6.3e-107;
Matches 234; Conservative 43; Mismatches 52; Indels 9; Gaps 3;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSVNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGLVQDYFPPPTVSVNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 116
DB 61 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 119

QY 117 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKP 176
DB 120 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHDEPEVKFNWYDGVGVHNAKTKP 179

QY 177 REQVNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 236
DB 180 KEQVNSTYRVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 239

QY 237 PPSRDELTQKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 294
DB 240 APHPDELKSKSVTVCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLK 299

QY 295 LTVDKSRNQGVNFCVSNVHNAKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 332
DB 300 LTVDKSRNQGVNFCVSNVHNAKNTKVDKKVPEKSCDKHTHTCCPCPAPELGG 337

RESULT 6
Q96P08
ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Factor VII active site mutant immunocorjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98; 12180-12185 (2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF272774; AAK58686.1; -.
DR HSSP; P00761; 1AN1.
DR InterPro; IPR000152; Asx_hydroxyl.
```


Best Local Similarity 62.7%; Pred. No. 1.4e-96;
Matches 208; Conservative 55; Mismatches 59; Indels 10; Gaps 4;

```
QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62
Db 140 AKTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 199
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPSNTKVDKVEPKSCDKHTCTCP--CPAPELL 120
Db 200 -LYTSSSVTVPSSTWSEPTVTCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 253
QY 121 GGPVSFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180
Db 254 --SSVEIFPPKPKDVLITLTPKVTCTVVDISKDDPEVQFSWFVDVEVHTAQTQPREEQ 311
QY 181 YNSTYRVSVLTVLHODWLNKEVKCKVSNKALPAPIETKISKAKGQPREPOVYITLPPSR 240
Db 312 FNSTFRSVELPIHQDWLNKEFKCRVNSAFAPIETKISKGRPKAPQVYITLPPPK 371
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK 300
Db 372 EQMAKDKVSLTCLMTDFPEDITVWQWNGQPAENYKNTQPIMDTDSGYFVYKLVNQKS 431
QY 301 RWQGNVPSCSVMHEALHNHYTQKSLSLSPGK 332
Db 432 NWEAGNTFTCSVLHGLHNHTKLSLSPGK 463
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RESULT 9

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Q9R1A4 PRELIMINARY; PRT; 437 AA.
ID Q9R1A4
AC Q9R1A4
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Gammaal heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)".
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; F01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh_4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; Igh LIKE; 4.
DR PROSITE; PS00290; Igh MHC; 1.
FT NON TER 1
FT NON TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B3BE7D697C CRC64;
```

Query Match 64.7%; Score 1151; DB 11; Length 437;
Best Local Similarity 62.3%; Pred. No. 2.9e-96;
Matches 207; Conservative 56; Mismatches 59; Indels 10; Gaps 4;

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QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62
Db 114 AKTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 173
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPSNTKVDKVEPKSCDKHTCTCP--CPAPELL 120
Db 174 -LYTSSSVTVPSSTWSEPTVTCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 227
```

```
QY 121 GGPVSFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 180
Db 228 --SSVEIFPPKPKDVLITLTPKVTCTVVDISKDDPEVQFSWFVDVEVHTAQTQPREEQ 285
QY 181 YNSTYRVSVLTVLHODWLNKEVKCKVSNKALPAPIETKISKAKGQPREPOVYITLPPSR 240
Db 286 FNSTFRSVELPIHQDWLNKEFKCRVNSAFAPIETKISKGRPKAPQVYITLPPPK 345
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDK 300
Db 346 EQMAKDKVSLTCLMTDFPEDITVWQWNGQPAENYKNTQPIMDTDSGYFVYKLVNQKS 405
QY 301 RWQGNVPSCSVMHEALHNHYTQKSLSLSPGK 332
Db 406 NWEAGNTFTCSVLHGLHNHTKLSLSPGK 437
```

RESULT 10

```
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4
AC Q9D8L4
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE 1810060009rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085860; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Offelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; F01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh_4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; Igh LIKE; 4.
DR PROSITE; PS00290; Igh MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 90ED57A514475FBB CRC64;
```

Query Match 64.0%; Score 1137.5; DB 11; Length 473;

Best Local Similarity 61.9%; Pred. No. 5.5e-95;
Matches 208; Conservative 53; Mismatches 68; Indels 7; Gaps 2;

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QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNGALTSYGHTTPAVLQSS 62
Db 114 AKTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGHTTPAVLQSD 173
QY 63 GLYSLSVVTVPSSSLGQTQYICNNHKPSNTKVDKVEPKSCDKHTCTCP--CPAPELL 120
Db 174 -LYTSSSVTVPSSTWSEPTVTCNVAHPASSTKVDKIVPRDCG----CKPCICTVPEV- 227
```

```
Db 139 AKTAPSVVPLAPVCGGTTGGTSSVTGLCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 197
QY 63 GLYSLSVVTVPSSSSLGTQTYICNVNHKPSNTKYDKVPEPK-----SCDKTHICPPCPA 116
Db 198 GLYTLSSSVTVTSNTWPSQITICNVAHPASSTKYDKKIEPRVPIITQNCPPLKCEPCPCAA 257
QY 117 PELLGGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 176
Db 258 PELLGGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 317
QY 177 REEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYTL 236
Db 318 HREDYNTSLRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYTL 377
QY 237 PPSRDLSTKQVSLTCLVKGYFSPDSIAVEHESNGOPENNYKTTTPVLDSDGSFPLYSKLT 296
Db 378 PPAEEMTKKPSLTCMIGTGPFAETAVDWTNSGRTEQNYKNTAIVLDSGDSYFMYSKLR 437
QY 297 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 438 VDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 473

RESULT 11
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 63.1%; Score 1122; DB 11; Length 468;
Best Local Similarity 63.6%; Pred. No. 1.4e-93;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGSPVFLPAPSSKSTGGTAALCLVKDYFPEPVTVWNSGALTSGVHTFPAVLQSS 62
Db 139 AKTAPSVVPLAPVCGDITGGSSVTGLCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 198
QY 63 GLYSLSVVTVPSSSSLGTQTYICNVNHKPSNTKYDKVPEPKCDKTHICPP--CPAPELL 120
Db 199 -LYTLSSSVTVTSWPSGSIICNVAHPASSTKYDKKIEPRG-PTIKPCPPCKCPAPNLL 256
QY 121 GGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 180
Db 257 GGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 316
QY 181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYTLPPSR 240
Db 317 YNSTLRVVSALP*IQHQQWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPE 376
QY 241 DELTKQVSLTCLVKGYFSPDSIAVEHESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKS 300
Db 377 EEMTKQVTLTCNVTFMPEDIVVWNTNGKTELNTPEVLDSDGSYFMYSKLRVEKK 436
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QY 301 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 437 NWVERNSYSCSVVHGLEHNNHTTKSPSRTPGK 468

RESULT 12
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.1%; Score 1122; DB 11; Length 473;
Best Local Similarity 63.6%; Pred. No. 1.4e-93;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 3 ASTKGSPVFLPAPSSKSTGGTAALCLVKDYFPEPVTVWNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVVPLAPVCGDITGGSSVTGLCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSD 203
QY 63 GLYSLSVVTVPSSSSLGTQTYICNVNHKPSNTKYDKVPEPKCDKTHICPP--CPAPELL 120
Db 204 -LYTLSSSVTVTSWPSGSIICNVAHPASSTKYDKKIEPRG-PTIKPCPPCKCPAPNLL 261
QY 121 GGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 180
Db 262 GGPSVFLFPKPKD*TLMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 321
QY 181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYTLPPSR 240
Db 322 YNSTLRVVSALP*IQHQQWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPE 381
QY 241 DELTKQVSLTCLVKGYFSPDSIAVEHESNGOPENNYKTTTPVLDSDGSFPLYSKLTVDKS 300
Db 382 EEMTKQVTLTCNVTFMPEDIVVWNTNGKTELNTPEVLDSDGSYFMYSKLRVEKK 441
QY 301 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
Db 442 NWVERNSYSCSVVHGLEHNNHTTKSPSRTPGK 473

RESULT 13
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH0327.1; -.
DR MGD; MGI:2144967; AU044919.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F0099332AF12 CRC64;

Query Match 61.2%; Score 1088; DB 11; Length 473;
Best Local Similarity 60.8%; Pred. No. 1.8e-90;
Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 138 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYFPEPVTVSWNSGSLSSVHTFPAVLQ-S 196

QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKT-HTCPP-----CP 115
DB 197 GLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPSGPISTINPCPCKECHKCP 256

QY 116 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175
DB 257 APNLEGGPSVFIFPPNPKDVLMLSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEVHTAQ 316

QY 176 PREEQYNSTYRVVSVLTVHLQDWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYT 235
DB 317 THREDYNSTIRVVSALPFOHQDWMSGKFKCKVNNKDLPSPIRTISKIKGLVRAPQVYI 376

QY 236 LPSPRDELTKNOVSLTCLVKGYPVDIAVEWESNGQPNENYKTPPVLDSDGSGFFLYSKL 295
DB 377 LPPPAEQLRKDVSLTCLVGVNPGDISVWTSNGHTENYKDTAPVLDSDGSGFFLYSKL 436

QY 296 TVDKSRWQGNVFCSCVMEALHNYTKLSLSLSPGK 332
DB 437 DIKTSKWEKTSFSCNVRHEGLKNLYLKTIISRSPOK 473

RESULT 14
QY Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.7 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 61.2%; Score 1088; DB 11; Length 474;
Best Local Similarity 60.8%; Pred. No. 1.8e-90;
Matches 205; Conservative 49; Mismatches 75; Indels 8; Gaps 3;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 139 AKTTPSVYPLAPGCGDTGSSVTLGCLVKGYFPEPVTVSWNSGSLSSVHTFPAVLQ-S 197

QY 63 GLYSLSVVTVPPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKT-HTCPP-----CP 115
DB 198 GLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDKLEPSGPISTINPCPCKECHKCP 257

QY 116 APELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175
DB 258 APNLEGGPSVFIFPPNPKDVLMLSLTPKVTCTVVDVSEDDPDVQISWFFVNNVEVHTAQ 317

QY 176 PREEQYNSTYRVVSVLTVHLQDWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYT 235
DB 318 THREDYNSTIRVVSALPFOHQDWMSGKFKCKVNNKDLPSPIRTISKIKGLVRAPQVYI 377

QY 236 LPSPRDELTKNOVSLTCLVKGYPVDIAVEWESNGQPNENYKTPPVLDSDGSGFFLYSKL 295
DB 378 LPPPAEQLRKDVSLTCLVGVNPGDISVWTSNGHTENYKDTAPVLDSDGSGFFLYSKL 437

QY 296 TVDKSRWQGNVFCSCVMEALHNYTKLSLSLSPGK 332
DB 438 DIKTSKWEKTSFSCNVRHEGLKNLYLKTIISRSPOK 474

RESULT 15
QY Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7B055851 CRC64;

Query Match 25.0%; Score 444.5; DB 4; Length 597;
Best Local Similarity 26.5%; Pred. No. 8.8e-32;
Matches 116; Conservative 68; Mismatches 142; Indels 111; Gaps 15;

QY 4 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 60
DB 146 SASAPFLFPLVSCNSPSTSSVAVGCLAQDPLDPSITTSWKYKNSDSSITGFGFSLR 205

QY 61 SSGLYSLSSVVTVPPSSSL--GQTY-ICNVNHPKSN-----TKVDKVEPK 103

```
Db 206 -GGKYAATSQVLLPSKDVNQGTDEHVVKVQHPNGNKKKNVLPFVIALPPKVSFVFP 264
QY 104 S-----CDKHTCP-----PCPAPELLGSPS----- 124
Db 265 DGFFGNPRKSLICQATGSPRQIOVSWMLREGKQVSGVTTDQVQAEAKESGPTTYKVT 324
QY 125 -----VPLFPKPKDTILMISRT 141
Db 325 TITIKESDWLSQSMFTCRVDHRLTFQQNASSMVCVDDQDTAIRVFAIPPS-FASIFLTKS 383
QY 142 PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVWSVLTVLHQDWLNG 201
Db 384 TKLTCIVTDLTTVD-SVTISWTRQNGEAVKTHNISESHPNATPSAVGEASICEDDWSG 442
QY 202 KEYCKKVSNAKLPAPIEKTIKAKGOP-REPOVYTLPPSRDELT-KNOVSLTCLVKGFYP 259
Db 443 ERFTCTVHTDLPSPKQKQISRPKGVALLHRLPDVYLLPPAREQLNRESATITCLVTGFS 502
QY 260 SDIAVESWESNGOP--ENNYKTPPVLD--SDGSFELYSKLTVDKSRMQGNVFCVSMHE 315
Db 503 ADVFVQWQWQGOPLSPKQVTSAPWPEQAPGRYFAHSILITVSEBEKNGTGETYTCVVAHE 562
QY 316 ALHNHYTQKSLSLSPGK 332
Db 563 ALPNRVTERTVDKSTGK 579
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Search completed: January 13, 2004, 12:43:09
Job time : 60.441 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 77.4183 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASKGPSVFLAPSSKST.....MHEALHNYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1773	99.7	534	13 AAR26531
2	1767	99.4	330	22 AAB04071
3	1767	99.4	330	23 ABB81641
4	1767	99.4	330	23 AAE21960
5	1767	99.4	330	23 ABB05736
6	1767	99.4	330	23 AAM47856
7	1767	99.4	330	24 ABB71856
8	1767	99.4	330	24 AAE32627
9	1767	99.4	330	24 AAE32915

10	1767	99.4	351	14 AAR43685	Human kappa immuno
11	1767	99.4	371	10 AAP91918	Sequence of the li
12	1767	99.4	442	24 ABB80109	Heavy chain. Homo
13	1767	99.4	442	24 ABB80113	Deglycosylated hea
14	1767	99.4	442	24 ABR39485	Humanised anti-Abe
15	1767	99.4	442	24 ABR39474	Humanised anti-Abe
16	1767	99.4	442	24 ABU08311	Humanised 266 anti
17	1767	99.4	442	24 ABU08320	Humanised antibody
18	1767	99.4	444	24 AAE34876	BIWA4/8 antibody h
19	1767	99.4	447	20 AAY31669	Human IGG1 chain C
20	1767	99.4	448	23 AAM49203	Humanised monoclon
21	1767	99.4	449	14 AAR43339	Completely humanis
22	1767	99.4	449	19 AAM49816	Amino acid sequenc
23	1767	99.4	449	24 ABF58273	Humanised 3D6 anti
24	1767	99.4	450	24 ABG74713	Murine humanised M
25	1767	99.4	451	22 AAE12715	Human recombinant
26	1767	99.4	451	24 ABU58807	Mucin 1 (MUC-1) bi
27	1767	99.4	452	20 AAY30201	Heavy chain sequen
28	1767	99.4	453	24 ABP96295	4A5-3.1.1-B4 antib
29	1767	99.4	453	24 ABP58287	Humanised 10D5 ant
30	1767	99.4	461	14 AAR42162	Anti-HIV-1 recombi
31	1767	99.4	461	22 AAU07745	Humanised monoclon
32	1767	99.4	465	22 AAB72228	Reshaped CD4 antib
33	1767	99.4	467	13 AAR22758	Humanised 323/A3 (
34	1767	99.4	467	13 AAR22759	Reshaped CD4 antib
35	1767	99.4	468	23 AAR27928	Human C5E10 antibo
36	1767	99.4	468	24 ABB82837	Antibody C5E10 hea
37	1767	99.4	470	13 ABP58275	Humanised 3D6 anti
38	1767	99.4	470	21 AAU7289	Reshaped CAMPATH-1
39	1767	99.4	470	21 AAU7289	Protein #2 in inve
40	1767	99.4	472	24 ABP58289	Humanised 10D5 ant
41	1767	99.4	473	22 AAG64469	Human type antiHum
42	1767	99.4	473	22 AAG64471	Human type antiHum
43	1767	99.4	473	22 AAG64473	Human type antiHum
44	1767	99.4	473	22 AAG64475	Human type antiHum
45	1767	99.4	475	13 AAR20057	Heavy chain of 3D6

ALIGNMENTS

```
RESULT 1
AAR26531
ID AAR26531 standard; Protein; 534 AA.
XX
AC AAR26531;
XX
DT 25-MAR-2003 (updated)
DT 28-JAN-1993 (first entry)
XX
DE Sequence of CD4-IgG1 chimeric heavy chain heterotrimer.
XX
KW CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;
KW therapy; diagnostic agent; inhibition.
XX
OS Synthetic.
XX
FH Key Active-site
FT Region Location/Qualifiers
FT Region 205..302
FT Region /label= CH1
FT Region 303..317
FT Region /label= hinge
FT Region 318..427
FT Region /label= CH2
FT Region 428..534
FT Region /label= CH3
PN WO9213559-A1.
XX
PD 20-AUG-1992.
XX
PF 10-FEB-1992; 92MO-US01152.
```

KW 08-FEB-1991; 91US-0654205.
 XX (PROG-) PROGENICS PHARM INC.
 XX Beaudry GA, Maddon RJ;
 XX WPI; 1992-299758/36.
 DR N-PSDB; AA027831.
 XX
 XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression
 PT vector - for preventing and treating HIV infection useful as a
 PT diagnostic agent
 XX
 XX Example; Fig 4; 88pp; English.
 XX
 CC The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned
 CC into M13mp18. In order to excise a fragment containing the CH1
 CC exon of the human gamma 1 heavy chain gene, the plasmid pBR
 CC gamma 1 is digested with SacII and the SacII sites are then
 CC made flush using T4 DNA polymerase. The fragment containing
 CC the CH1 exon is then purified and ligated to the M13mp18(CD4)
 CC vector. Oligonucleotide-mediated site-directed mutagenesis is then
 CC performed to juxtapose the CD4 and CH1 sequences in frame. The
 CC CD4-CH1 chimeric gene is then linearized and ligated to the
 CC Pet1-Pst1 DNA fragment of the plasmid pBR gamma 1 containing the
 CC hinge, CH2, and CH3 exons of the human gamma 1 chain gene
 CC designated CD4-IgG1HC-pRCMV (ATCC 75192).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 534 AA;
 XX
 Query Match 99.7%; Score 1773; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 2.4e-125;
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 61
 DB 204 FASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 61
 QY 62 SGLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLG 121
 DB 264 SGLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLG 323
 QY 122 GSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQY 181
 DB 324 GSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQY 383
 QY 182 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 241
 DB 384 NSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 443
 QY 242 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSR 301
 DB 444 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKSR 503
 QY 302 WQGGVFNVCNVHEALHNHYTQKSLSLSPGK 332
 DB 504 WQGGVFNVCNVHEALHNHYTQKSLSLSPGK 534
 RESULT 2
 AAB04071
 ID AAB04071 standard; Protein; 330 AA.
 XX
 AC AAB04071;
 XX
 DT 11-APR-2001 (first entry)
 XX
 DE Zcytor 10::IgG gamma fusion peptide.
 XX
 DE zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
 KW binding; detection; modulation; recombinant cell;
 KW

KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;
 KW immune system; blood; bone; inflammatory response; inflammation;
 KW spleen; human.
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO2000068381-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 11-MAY-2000; 2000WO-US12924.
 XX
 XX 11-MAY-1999; 99US-0309861.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Presnell SR, Foster DC, Hammond AK, Lok S;
 XX
 XX WPI; 2001-016096/02.
 XX
 XX N-PSDB; AAA54473.
 XX
 XX New cytokine receptor mouse zcytor 10, useful for detecting ligands
 PT that stimulate proliferation or development of haematopoietic,
 PT lymphoid and myeloid cells
 XX
 XX Example 17; Page 120-121; 134pp; English.
 XX
 CC Isolating a nucleotide which encodes the zcytor 10 cytokine
 CC receptor enables the production of recombinant cells expressing the
 CC receptor. Those cells can then be used to detect the presence of a
 CC modulator of zcytor10 protein by culturing the cells in the presence
 CC of a test ligand and comparing levels of activity of mouse zcytor10
 CC in the presence and absence of the test sample. Similarly, detection
 CC of zcytor10 receptor ligand within a test sample can be achieved.
 CC The method comprising contacting a test sample containing an amino
 CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
 CC cytokine receptor and detecting the binding of the polypeptide to a
 CC ligand in the sample. Specified peptide fragments of the zcytor 10
 CC cytokine receptor and the methods described are used to identify
 CC ligands that stimulate the proliferation and/or development of
 CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
 CC the cytokine receptor are useful for treating lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders and for generating
 CC antibodies directed against the receptor. A vector expressing a
 CC secreted human zcytor 10 heterodimer is constructed. In this
 CC construct the extracellular cytokine binding domain of zcytor 10
 CC is fused to the heavy chain of IgG gamma and the extracellular
 CC portion of the heteromeric cytokine receptor subunit (an
 CC interleukin receptor subunit) is fused to human kappa light
 CC chain (See GENESEQ record AAA54474). The two sequences are fused
 CC together using two primers (AAA54475, AAA54476).
 XX
 XX Sequence 330 AA;
 XX
 Query Match 99.4%; Score 1767; DB 22; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-125;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 62
 DB 1 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
 QY 63 GLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLG 122
 DB 61 GLYSLSVVTVPPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLG 120
 QY 123 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQY 182
 DB 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQY 180
 QY 183 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 242

Db 181 STYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
 Db 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
 QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
 Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 3

ABBS1641
 ID ABB81641 standard; Protein: 330 AA.

XX AC ABB81641;

XX DT 25-SEP-2002 (first entry)

XX DE Human IgG gamma 1 heavy chain SEQ ID NO:15.

XX KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;

XX KW antitumetic; antiarthritic; neuroprotective; antiinflammatory;

XX KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;

XX KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;

XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;

XX KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;

XX KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;

XX KW mesangio proliferative disease; chronic lymphocytic leukaemia; bronchitis;

XX KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;

XX KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;

XX KW emphysema; chronic airway disease.

XX OS Homo sapiens.

XX XX WO2002424209-A2.

XX XX 06-JUN-2002.

XX XX 28-NOV-2001; 2001WO-US44808.

XX XX 28-NOV-2000; 2000US-253561P.

XX XX 07-FEB-2001; 2001US-267211P.

XX XX (ZYMO) ZYMOGENETICS INC.

XX XX Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FU;

XX XX WPI; 2002-527700/56.

XX XX N-PSDB; ABQ73076.

XX XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating

XX XX immune responses in animals for producing antibodies, and for treating

XX XX autoimmune diseases, leukemia and asthma -

XX XX Example 7; Page 171-172; 200pp; English.

XX XX The present invention describes an isolated human zcytor19 protein (I),

XX XX and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,

XX XX antitumetic, antiarthritic, neuroprotective, antiinflammatory,

XX XX antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic

XX XX activities, and can be used in vaccines. (I) or an antibody binding (I)

XX XX can be used for suppressing the immune system for reducing rejection of

XX XX tissue or organ transplants and grafts and for treating T-cell specific

XX XX leukaemias or lymphomas and autoimmune diseases including rheumatoid

XX XX arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel

XX XX disease and Crohn's disease. The antibodies can also be used for treating

XX XX immunologic renal diseases, glomerulonephritis, mesangio proliferative

XX XX disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or

XX XX vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related

XX XX diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the

XX XX antibodies can also be used for renal or urological neoplasms and

XX XX multiple myelomas, asthma, bronchitis, emphysema and other chronic

CC CC CC CC CC
 CC specifically to chromosome 1p36.11. The present sequence represents
 CC a human IGG gamma 1 heavy chain protein, which is used in an example
 CC from the present invention.
 XX XX

SQ Sequence 330 AA;

Query Match 99.4%; Score 1767; DB 23; Length 330;

Best Local Similarity 100.0%; Pred. No. 3.7e-125;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 122

Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHCTCPPELGG 120

QY 123 PSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQVGEVHNAAKTPREBOYN 182

Db 121 PSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQVGEVHNAAKTPREBOYN 180

QY 183 STYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242

Db 181 STYRWSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302

Db 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332

Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 4

AAE21960

ID AAE21960 standard; Protein: 330 AA.

XX AC AAE21960;

XX DT 25-JUL-2002 (first entry)

XX DE Human death domain containing receptor (DR6) protein-related protein.

XX KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;

XX KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;

XX KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;

XX KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;

XX KW autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;

XX KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;

XX KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;

XX KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;

XX KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;

XX KW dermatological; hepatotropic; antibacterial.

XX OS Homo sapiens.

XX XX WO200185209-A2.

XX XX 15-NOV-2001.

XX XX 30-APR-2001; 2001WO-US11735.

XX XX 10-MAY-2000; 2000US-203015P.

XX XX (ELIL) LILLY & CO ELI.

XX XX Heuer JG, Liu J, Na S, Song HY, Yang D;

XX XX WPI; 2002-351283/38.

QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETIISKAKQPREPOVYTLPPSRDE 242
 DB 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETIISKAKQPREPOVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 303 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 332
 DB 301 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 330

RESULT 6

AAM47856

ID AAM47856 standard; Protein; 330 AA.

XX AC AAM47856;

XX DT 22-FEB-2002 (first entry)

XX DE Human Ig-gammal heavy chain constant region amino acid sequence.

XX KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;

XX KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;

XX KW transgenic plant.

XX OS Homo sapiens.

XX PN WO2001183529-A2.

XX PD 08-NOV-2001.

XX PF 28-APR-2001; 2001WO-US13932.

XX PR 28-APR-2000; 2000US-200298P.

XX PA (PLAN-) PLANET BIOTECHNOLOGY INC.

XX PI Larrick JW, Wycoff KL;

XX DR WPI; 2002-041481/05.

XX DR N-PSDB; ABA05265.

XX PT Immunoadhesin for treating human rhinovirus infection comprises

XX PT chimeric intercellular adhesion molecule-1, and optionally a J chain

XX PT and secretory component in association

XX PS Disclosure; Fig 7; 138pp; English.

XX CC The invention relates to an immunoadhesin comprising:

XX CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a

XX CC rhinovirus receptor protein linked to at least a portion of an

XX CC immunoglobulin heavy chain; and

XX CC (b) optionally a J chain and secretory component associated with the

XX CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific

XX CC glycosylation and virucide activity. The immunoadhesin is useful for

XX CC reducing infection by human rhinovirus (HRV) and hence the initiation or

XX CC spread of the common cold by HRV. The immunoadhesin binds to HRV and

XX CC reduces its infectivity, competing with cell surface ICAM-1 for binding

XX CC sites, interfering with virus entry or uncoating and directing premature

XX CC release of viral RNA and formation of empty capsids. Expression of the

XX CC immunoadhesin in plants would be tetrameric, rather than dimeric.

XX CC Immunoadhesin having multiple binding sites have a higher effective

XX CC affinity for the virus, thereby increasing the effectiveness of the

XX CC immunoadhesin. Association of secretory component and immunoglobulin J

XX CC chain increases the stability of the immunoadhesin in the mucosal

XX CC environment. Production is significantly less expensive in plants than in

XX CC animal cell culture and production in plants is safer for human use,

XX CC since plants are not known to harbor any animal viruses. The present

XX CC sequence is that of a human immunoglobulin protein sequence, useful to

XX CC the invention.

XX SQ Sequence 330 AA;
 Query Match 99.4%; Score 1767; DB 23; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0;
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCTCPCPAPELGG 122
 DB 61 GLYSLSSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCTCPCPAPELGG 120
 QY 123 PSVFLFPPPKDTLMISRTPEVTCVVDVSHEDDEVKFNWYVDGVEVHNNAKTKPREEOYN 182
 DB 121 PSVFLFPPPKDTLMISRTPEVTCVVDVSHEDDEVKFNWYVDGVEVHNNAKTKPREEOYN 180
 QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETIISKAKQPREPOVYTLPPSRDE 242
 DB 181 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETIISKAKQPREPOVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 303 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 332
 DB 301 QQGNVFCSCVMHEALHNHYTKSLSLSPGK 330

RESULT 7

ABP71856

ID ABP71856 standard; protein; 330 AA.

XX AC ABP71856;

XX DT 17-APR-2003 (first entry)

XX DE Human IgG1 Fc gamma region.

XX KW Human; fusion protein; IgE Fc epsilon; IgG Fc gamma; Fc epsilonRI; allergy;

XX KW Fc epsilonRII; Fc gammaRII; protein therapy; IGE; IgG; asthma; hay fever;

XX KW allergic asthma; allergic rhinitis; hay fever; food allergy;

XX KW atopic dermatitis; drug allergy; peanut allergen.

XX OS Homo sapiens.

XX PH Key

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

XX FT Region

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XX FT Region

PT New fusion protein which binds to FcεpsilonRI or RII receptor and
 PT FcγmαRIIB receptor, useful for treating or preventing allergies and
 PT asthma, comprises an IGE FcεpsilonI fragment and an IGE Fcγmα fragment
 PT -
 XX Disclosure; Fig 5; 32pp; English.

XX The invention relates to a novel fusion protein comprising an IGE
 CC FcεpsilonI fragment and an IGE Fcγmα fragment, which binds to an
 CC FcεpsilonRI and/or FcεpsilonRII receptor and an FcγmαRIIB receptor. The
 CC fusion protein of the invention may have a use in protein therapy. The
 CC fusion protein is useful in treating or preventing IGE-mediated allergies
 CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food
 CC allergy, atopic dermatitis and drug allergy. The allergic response is
 CC particularly caused by peanut allergen. The present sequence represents
 CC the human IGE1 Fcγmα fragment.

XX Sequence 330 AA;

Query Match 99.4%; Score 1767; DB 24; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELGG 122
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELGG 120
 QY 123 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 DB 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 QY 183 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 DB 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
 QY 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332
 DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 8

AAE32627
 ID AAE32627 standard; Protein; 330 AA.

AC AAE32627;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

DE Human; immunogenic; therapy; immunoglobulin G1; IgG1.

XX Homo sapiens.

XX WO200279415-A2.

XX 10-OCT-2002.

XX 29-MAR-2002; 2002WO-US09650.

XX 30-MAR-2001; 2001US-280625P.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD;

XX WPI; 2003-111794/10.

XX Reducing the immunogenicity of a fusion protein by changing an amino
 PT acid within the junction region spanning a fusion junction of a fusion
 PT protein to reduce the ability of the candidate T-cell epitope to
 PT interact with a T-cell receptor -
 XX Disclosure; Page 49-50; 67pp; English.

XX The present invention relates to a method of reducing the immunogenicity
 CC of a fusion protein. The method involves identifying a candidate T-cell
 CC epitope within a junction region spanning a fusion junction of a T-cell
 CC protein and changing an amino acid within the junction region to reduce
 CC the ability of the candidate T-cell epitope to interact with a T-cell
 CC receptor. The method is useful for reducing the immunogenicity of fusion
 CC proteins for use in therapy. The present sequence is human immunoglobulin
 CC G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the
 CC method of the invention.

XX Sequence 330 AA;

Query Match 99.4%; Score 1767; DB 24; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3.7e-125; Indels 0; Gaps 0;
 Matches 330; Conservative 0; Mismatches 0;

QY 3 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELGG 122
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELGG 120
 QY 123 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 DB 121 PSVFLPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 QY 183 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 DB 181 STYRVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDKSRW 300
 QY 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332
 DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 9

AAE32915
 ID AAE32915 standard; Protein; 330 AA.

AC AAE32915;

DT 24-MAR-2003 (first entry)

DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.

XX T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.

XX Homo sapiens.

XX WO200279232-A2.

XX 10-OCT-2002.

XX 30-MAR-2002; 2002WO-US09815.

XX 30-MAR-2001; 2001US-280625P.

XX

PA (LEXI-) LEXIGEN PHARM CORP.
 XX Gillies SD;
 XX WPI; 2003-103259/09.
 XX Reducing the immunogenicity of a fusion protein comprises changing an
 PT amino acid within the junction region to reduce the ability of the
 PT candidate T-cell epitope identified within the junction spanning to
 PT interact with T-cell receptor -
 XX
 XX Disclosure; Page 49-50; 68pp; English.
 XX The invention relates to a method for reducing the immunogenicity of a
 CC fusion protein which involves identifying a candidate T-cell epitope
 CC within a junction spanning a fusion junction of a fusion protein, and
 CC changing an amino acid within the junction region to reduce the ability
 CC of the candidate T-cell epitope to interact with a T-cell receptor. The
 CC method is useful for reducing the immunogenicity of a fusion protein.
 CC It is useful for analysing, changing or modifying one or more amino
 CC acids in the junction region of a fusion protein to identify a T-cell
 CC epitope and reduce its ability to interact with a T-cell receptor. The
 CC less immunogenic fusion proteins are useful in providing therapeutic
 CC treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy
 CC chain Fc region used to illustrate the method of the invention.
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 99.4%; Score 1767; DB 24; Length 330;
 Best Local Similarity 100.0%; Pred. No. 3,7e-125;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 Db 1 ASTKGSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 122
 Db 61 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120
 QY 123 PSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 Db 121 PSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 QY 183 STYRVSVLTLVHQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
 Db 181 STYRVSVLTLVHQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
 QY 303 QGQNVFSCSVMEALHNYTKQSLSPGK 332
 Db 301 QGQNVFSCSVMEALHNYTKQSLSPGK 330

RESULT 10

AAR43685

ID AAR43685 standard; Protein; 351 AA.

XX AAR43685;

AC AAR43685;

XX 25-MAR-2003 (updated)

DT 25-MAY-1994 (first entry)

XX

DE Human kappa immunoglobulin light chain constant domain.

XX Human; immunoglobulin; constant; region; humanised; P-selectin; light;
 KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;
 KW monoclonal; PBI.3; CDR; complementarity determining region; leukocyte;
 KW expression vector; coexpression; pHCMV-1748HA-gamma1ci-dhfr; epitope;
 KW pHCMV-1748HA-KR-neo; PBI.3/Humanised version A; vascular endothelium;

KW pHCMV-1747CH-gamma1ci-neo; pHCMV-1747-CL-KR-neo; PBI.3 chimera;
 KW acute lung injury; ischaemia reperfusion injury; inflammation.
 XX Homo sapiens.
 OS
 XX
 PH Key Location/Qualifiers
 FT Domain 22..119
 FT /note= "CH1 domain"
 FT Region 120..134
 FT /note= "Hinge region"
 FT Domain 135..244
 FT /note= "CH2 domain"
 FT Domain 245..352
 FT /note= "CH3 domain"
 XX
 PN W09321956-A1.
 XX
 PD 11-NOV-1993.
 XX
 PP 04-MAY-1993; 93WO-US04274.
 XX
 PR 05-MAY-1992; 92US-0880196.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 XX Chestnut RW, Paulson JC, Polley MJ;
 XX
 DR WPI; 1993-368423/46.
 DR N-PSDB; AAQ51547.
 XX
 PT Anti-P-selectin antibody for ischaemia acute lung injury treatment -
 PT useful to treat inflammation and pathological conditions of
 PT intercellular adhesion by competitive inhibition assays
 XX
 PS Example 10; Fig 9; 82pp; English.
 XX
 CC The sequences given in AAR43685-86 represent human immunoglobulin
 CC constant regions which were used in the production of the humanised
 CC P-selectin blocking antibody, along with the heavy and light chain
 CC variable region coding sequences of the murine monoclonal antibody
 CC PBI.3. Given in AAR43687-88. The CDRs from PBI.3 heavy and light
 CC chains were substituted for the CDRs of human heavy and light chains.
 CC The humanised variable regions were inserted into expression vectors.
 CC By coexpression of appropriate combinations of heavy and light
 CC chains, several humanised antibodies can be expressed. Coexpression
 CC of pHCMV-1748HA-gamma1ci-dhfr and pHCMV-1748HA-KR-neo gives rise
 CC to the PBI.3/Humanised version A. Coexpression of pHCMV-1747CH-
 CC gamma1ci-neo and pHCMV-1747-CL-KR-neo gives rise to the PBI.3 chimera.
 CC These humanised antibodies selectively bind epitopes on P-selectin and
 CC block adhesion of leukocytes to the vascular endothelium. They may be
 CC used to treat inflammatory and thrombotic diseases and other
 CC pathological conditions involving P-selectin and antibodies to it, esp.
 CC acute lung injury and ischaemia reperfusion injury.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 351 AA;

Query Match

99.4%; Score 1767; DB 14; Length 351;

Best Local Similarity 100.0%; Pred. No. 3.9e-125;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62

Db 22 ASTKGSVFFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 81

QY 63 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 122

Db 82 GLYSLSVWTVVPSSSLGTQYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 141

QY 123 PSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182

Db 142 PSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 201

QY 183 STYRVSVLTVLHODWLNKKEYCKYSNKKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 Db 202 STYRVSVLTVLHODWLNKKEYCKYSNKKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 261
 QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
 Db 262 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 321
 QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
 Db 322 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 351

RESULT 11
 AAP91918
 ID AAP91918 standard; protein; 371 AA.
 XX AC AAP91918;
 XX DT 25-MAR-2003 (updated)
 DT 31-OCT-2002 (updated)
 DT 14-MAY-1990 (first entry)
 XX
 DE Sequence of the linked immunoglobulin gamma chain fragment.
 XX Immunoglobulin gamma chain; IgG1 heavy chain constant region.
 KW
 XX Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Misc-difference 42..43 /note= "Insert site"
 FT Misc-difference 144..145 /note= "Insert site"
 FT
 XX EP314317-A.
 XX 03-MAY-1989.
 PD
 XX 03-OCT-1988; 88EP-0309194.
 XX 02-OCT-1987; 87US-0104329.
 PR 28-SEP-1988; 88US-0250785.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Capon DJ, Gregory TJ;
 XX WPI; 1989-131855/18.
 DR N-PSDB; AAN90779.
 XX
 PT Compans. contg. adhesion variants
 PT - useful in therapy and diagnostics, eg CD4 variants
 PT which are therapeutically useful for treating human
 PT immuno-deficiency virus
 XX
 PS Disclosure; Fig 4a-4b; 36pp; English.
 XX
 CC It may be fused to the first 180 N-terminal
 CC residues of CD4 at the C-terminus. The fusion protein may be used for
 CC antiviral of immunomodulatory therapy particularly in treatment of HIV
 CC infection.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 371 AA;
 Query Match 99.4%; Score 1767; DB 10; Length 371;
 Best Local Similarity 100.0%; Pred. No. 4.2e-125;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62

Db 42 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 101
 QY 63 GLYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKHTCTCPCPAPPELLGG 122
 Db 102 GLYSLSVWTVTPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKHTCTCPCPAPPELLGG 161
 QY 123 PSVFLPPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 Db 162 PSVFLPPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
 QY 183 STYRVSVLTVLHODWLNKKEYCKYSNKKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 Db 222 STYRVSVLTVLHODWLNKKEYCKYSNKKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 281
 QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
 Db 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 341
 QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
 Db 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

RESULT 12
 ABB80109
 ID ABB80109 standard; Protein; 442 AA.
 XX AC ABB80109;
 XX DT 13-JUN-2003 (first entry)
 XX DE Heavy chain.
 XX KW Complementarity determining region; CDR; humanised; mouse;
 KW 266; light; heavy; variable; domain; antibody; preclinical; clinical;
 KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
 KW central nervous system; plasma.
 XX Homo sapiens.
 OS Mus musculus.
 XX WO2003015617-A2.
 XX 27-FEB-2003.
 XX 16-AUG-2002; 2002WO-US26321.
 XX 17-AUG-2001; 2001US-313221P.
 PR 17-AUG-2001; 2001US-313224P.
 PR 23-OCT-2001; 2001US-334987P.
 XX (UNIW) UNIV WASHINGTON.
 PA (ELIL) LILLY & CO ELI.
 XX Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;
 XX WFI; 2003-278505/27.
 XX
 PT Diagnosing preclinical or clinical Alzheimer's disease in a subject by
 PT administering an antibody which specifically binds an epitope -
 XX Disclosure; Page 15-16; 64pp; English.
 XX
 CC The sequences given in AAG80104-09 represent preferred antibodies
 CC of the invention. This sequence represents the preferred heavy
 CC chain. The humanised antibody of the invention may be used for
 CC diagnosing preclinical or clinical Alzheimer's disease. The antibody
 CC specifically binds an epitope, preferably the amyloid beta peptide
 CC (Abeta). The antibodies sequester Abeta from its bound, circulating
 CC form in blood and alter clearance of soluble and bound forms of Abeta
 CC in central nervous system and plasma. The antibodies specifically bind
 CC an epitope representing amino acids 13-28 of the Abeta molecule.

```

XX SQ      Sequence      442 AA;
      Query Match      99.4%; Score 1767; DB 24; Length 442;
      Best Local Similarity 100.0%; Pred. No. 5.3e-125;
      Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172
QY 63 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPCPAPELLGG 122
Db 173 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPCPAPELLGG 232
QY 123 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 233 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 292
QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 293 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 352
QY 243 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 353 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 412

QY 303 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 332
Db 413 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 442

RESULT 13
ABR80113
ID ABR80113 standard; Protein; 442 AA.
XX AC ABR80113;
XX DT 13-JUN-2003 (first entry)
XX DE Deglycosylated heavy chain.
XX KW Complementarity determining region; CDR; humanised; mouse;
XX KW 266; light; heavy; variable; domain; antibody; preclinical; clinical;
XX KW Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
XX KW central nervous system; plasma.
XX OS Homo sapiens.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 56 /label= Any amino acid
XX FT /note= "Provided that if Xaa57 is neither Asp nor
XX FT Pro and Xaa58 is Ser or Thr, then Xaa56 is not Asn"
XX FT Misc-difference 57 /label= Any amino acid
XX FT /note= "Provided that if Xaa56 is Asn and Xaa58
XX FT is Ser or Thr, then Xaa57 is Asp or Pro"
XX FT Misc-difference 58 /label= Any amino acid
XX FT /note= "Provided that if Xaa56 is Asn and Xaa57 is
XX FT neither Asp nor Pro, then Xaa58 is neither Ser nor Thr"
XX FN WO2003015617-A2.
XX PD 27-FEB-2003.
XX PF 16-AUG-2002; 2002WO-US26321.
XX PR 17-AUG-2001; 2001US-313221P.
XX PR 17-AUG-2001; 2001US-313224P.
XX PR 23-OCT-2001; 2001US-334987P.

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XX PA (UNIW ) UNIV WASHINGTON.
XX PI (ELIL ) LILLY & CO ELI.
XX PI Holtzman DM, Demattos R, Bales KR, Cummins DJ, Paul SM;
XX PI WPI; 2003-278505/27.
XX DR
XX FT Diagnosing preclinical or clinical Alzheimer's disease in a subject by
XX FT administering an antibody which specifically binds an epitope -
XX PS Claim 8; Page 20-22; 64pp; English.
XX CC This sequence represents the preferred heavy chain from a
XX CC deglycosylated version of the humanised mouse antibody 266
XX CC heavy chain of the invention. The antibody of the invention
XX CC specifically binds an epitope, preferably the amyloid beta
XX CC peptide (Abeta). The antibodies sequester Abeta from its bound,
XX CC circulating form in blood and alter clearance of soluble and bound
XX CC forms of Abeta in central nervous system and plasma. The antibodies
XX CC specifically bind an epitope representing amino acids 13-28 of the
XX CC Abeta molecule. Deglycosylation of the heavy chain CDR2, as in this
XX CC sequence, causes higher affinity for Abeta. The antibody of the
XX CC invention may be used for diagnosing preclinical or clinical Alzheimer's
XX CC disease.
XX SQ      Sequence      442 AA;
      Query Match      99.4%; Score 1767; DB 24; Length 442;
      Best Local Similarity 100.0%; Pred. No. 5.3e-125;
      Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172
QY 63 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPCPAPELLGG 122
Db 173 GLYSLSSVTVTPSSSLGQTQYICNVNHPKSTNTKVDKVEPKSCDKTHTCPCPAPELLGG 232
QY 123 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 233 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 292
QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 293 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 352
QY 243 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 353 LTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 412

QY 303 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 332
Db 413 QQGNVFCVSNVHEALHNHYTQKSLSLSPGK 442

RESULT 14
ABR39465
ID ABR39465 standard; protein; 442 AA.
XX AC ABR39465;
XX DT 12-JUN-2003 (first entry)
XX DE Humanised anti-Abeta antibody 266 heavy chain.
XX KW Amyloid-beta; Abeta; antibody 266; nontropic; neuroprotective; CDR;
XX KW immunostimulant.
XX OS Homo sapiens.
XX OS WO2003016467-A2.

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XX 27-FEB-2003.
 XX
 XX
 PF 14-AUG-2002; 2002WO-US21324.
 XX
 XX 17-AUG-2001; 2001US-313576P.
 PR 28-MAY-2002; 2002US-383851P.
 PR
 XX
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Bales KR., Paul SM;
 PI WPI; 2003-289975/28.
 XX
 XX Treating or reducing the progression of diseases associated with
 PT amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or
 PT mild cognitive impairment, comprises administering an anti-amyloid-beta
 PT peptide antibody -
 XX
 XX Disclosure; Page 20-22; 84pp; English.
 PS
 XX The invention relates to treating cognitive symptoms or reducing disease
 CC progression in a subject having a condition or disease associated with
 CC amyloid-beta peptide (Abeta). The method involves administering an amount
 CC of an anti-Abeta antibody that has greater affinity for soluble Abeta
 CC than 10⁻⁹ M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42
 CC higher than 10⁻⁹ M, or that has greater affinity for soluble Abeta
 CC than antibody 266 has. The method or the anti-Abeta antibody is useful in
 CC preparing a medicament for treating cognitive symptoms or reducing
 CC disease progression in a subject having a condition or disease associated
 CC with Abeta. The condition or disease is Alzheimer's disease, Down's
 CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild
 CC cognitive impairment. The present sequence represents a humanised
 CC anti-Abeta antibody 266 heavy chain.
 XX
 XX Sequence 442 AA;
 SQ

Query Match 99.4%; Score 1767; DB 24; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172
 QY 63 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 122
 Db 173 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 232
 QY 123 PSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 182
 Db 233 PSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYN 292
 QY 183 STYRVSVLTIVLQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 Db 293 STYRVSVLTIVLQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 352
 QY 243 LTKNQVSLTCLVKGPYSDIAVEVESNGQPENNYKTTPPVLDSGSPFLYSKLTVDKSRW 302
 Db 353 LTKNQVSLTCLVKGPYSDIAVEVESNGQPENNYKTTPPVLDSGSPFLYSKLTVDKSRW 412
 QY 303 QGQNVFSCVMHEALHNYTKQSLSPGK 332
 Db 413 QGQNVFSCVMHEALHNYTKQSLSPGK 442

RESULT 15
 ABR39474
 ID ABR39474 standard; protein; 442 AA.
 XX
 AC ABR39474;
 XX
 DT 12-JUN-2003 (first entry)

XX
 DE Humanised anti-Abeta antibody 266 analogue heavy chain.
 XX
 KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
 XX immunostimulant.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 56
 FT /note= "Xaa is any amino acid, provided that if Xaa at
 FT position 57 is neither Asp nor Pro and Xaa at position
 FT 59 is Ser or Thr, then Xaa at position 56 is not Asn"
 FT
 FT Misc-difference 57
 FT /note= "Xaa is any amino acid, provided that if Xaa at
 FT position 56 is Asn and Xaa at position 58 is Ser or Thr,
 FT then Xaa at position 57 is Asp or Pro"
 FT
 FT Misc-difference 58
 FT /note= "Xaa is any amino acid, provided that if Xaa at
 FT position 56 is Asn and Xaa at position 57 is neither Asp
 FT nor Pro, then Xaa at position 58 is neither Ser nor Thr"
 FT
 FN WO2003016467-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US21324.
 XX
 XX 17-AUG-2001; 2001US-313576P.
 PR 28-MAY-2002; 2002US-383851P.
 PR
 XX (ELIL) LILLY & CO ELI.
 PA
 XX Bales KR., Paul SM;
 PI WPI; 2003-289975/28.
 XX
 XX Treating or reducing the progression of diseases associated with
 PT amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or
 PT mild cognitive impairment, comprises administering an anti-amyloid-beta
 PT peptide antibody -
 XX
 XX Disclosure; Page 29-31; 84pp; English.
 PS
 XX The invention relates to treating cognitive symptoms or reducing disease
 CC progression in a subject having a condition or disease associated with
 CC amyloid-beta peptide (Abeta). The method involves administering an amount
 CC of an anti-Abeta antibody that has greater affinity for soluble Abeta
 CC than 10⁻⁹ M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42
 CC higher than 10⁻⁹ M, or that has greater affinity for soluble Abeta
 CC than antibody 266 has. The method or the anti-Abeta antibody is useful in
 CC preparing a medicament for treating cognitive symptoms or reducing
 CC disease progression in a subject having a condition or disease associated
 CC with Abeta. The condition or disease is Alzheimer's disease, Down's
 CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild
 CC cognitive impairment. The present sequence represents a preferred heavy
 CC chain of a humanised anti-Abeta antibody 266 analogue that has a high
 CC affinity for Abeta.
 XX
 SQ Sequence 442 AA;
 Query Match 99.4%; Score 1767; DB 24; Length 442;
 Best Local Similarity 100.0%; Pred. No. 5.3e-125;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 Db 113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 172
 QY 63 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 122
 Db 173 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 232

QY	123	PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYN	182
Db	233	PSVFLFPKPKDXTLMISRTPEVTCVVVDVSHEDPEVKFNWVVDGVEVHNAKTKPREEQYN	292
QY	183	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	242
Db	283	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	352
QY	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDKSRW	302
Db	353	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDKSRW	412
QY	303	QCGNVFSCSVMEALHNNHYTKOKSLSPGK	332
Db	413	QCGNVFSCSVMEALHNNHYTKOKSLSPGK	442

Search completed: January 13, 2004, 12:38:27
 Job time : 79.4183 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 53.062 Seconds
(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASKTGFVPLAPSSKST.....MHEALHNYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	332	11	US-09-990-586-98
2	1778	100.0	332	12	US-10-310-113-167
3	1778	100.0	332	12	US-10-230-680-98
4	1767	99.4	330	11	US-09-995-898A-15
5	1767	99.4	330	11	US-09-892-949-38
6	1767	99.4	330	12	US-10-112-582-1
7	1767	99.4	330	12	US-10-310-719-8
8	1767	99.4	330	12	US-10-310-231A-81
9	1767	99.4	330	14	US-10-047-542-20
10	1767	99.4	330	15	US-10-269-805-68
11	1767	99.4	371	12	US-10-097-044A-7
12	1767	99.4	444	15	US-10-150-475A-6
13	1767	99.4	445	12	US-10-320-231A-79
14	1767	99.4	447	11	US-09-256-156-1
15	1767	99.4	451	10	US-09-822-698A-26
					Sequence 98, Appl
					Sequence 167, Appl
					Sequence 98, Appl
					Sequence 15, Appl
					Sequence 38, Appl
					Sequence 1, Appl
					Sequence 8, Appl
					Sequence 81, Appl
					Sequence 20, Appl
					Sequence 68, Appl
					Sequence 7, Appl
					Sequence 6, Appl
					Sequence 79, Appl
					Sequence 1, Appl
					Sequence 26, Appl

16	1767	99.4	470	12	US-10-104-047-3730	Sequence 3730, Ap
17	1767	99.4	476	10	US-09-747-669-3	Sequence 3, Appl
18	1767	99.4	476	12	US-10-409-938-15	Sequence 15, Appl
19	1767	99.4	476	15	US-10-290-703-3	Sequence 3, Appl
20	1767	99.4	547	9	US-09-746-359A-54	Sequence 54, Appl
21	1767	99.4	567	10	US-09-825-561A-16	Sequence 16, Appl
22	1767	99.4	571	9	US-09-746-359A-53	Sequence 53, Appl
23	1767	99.4	731	10	US-09-825-012-46	Sequence 46, Appl
24	1767	99.4	741	10	US-09-825-012-55	Sequence 55, Appl
25	1767	99.4	951	10	US-09-935-868-9	Sequence 9, Appl
26	1767	99.4	951	12	US-10-282-182-9	Sequence 9, Appl
27	1767	99.4	951	15	US-10-287-035-9	Sequence 9, Appl
28	1763	99.2	475	9	US-09-740-002-27	Sequence 27, Appl
29	1763	99.2	476	10	US-09-948-429B-4	Sequence 4, Appl
30	1763	99.2	476	10	US-09-948-429B-12	Sequence 12, Appl
31	1763	99.2	476	12	US-10-124-807-4	Sequence 4, Appl
32	1763	99.2	476	12	US-10-124-807-12	Sequence 12, Appl
33	1763	99.2	476	12	US-10-291-532-4	Sequence 4, Appl
34	1763	99.2	476	12	US-10-291-532-12	Sequence 12, Appl
35	1763	99.2	476	14	US-10-124-905-4	Sequence 4, Appl
36	1763	99.2	476	14	US-10-124-905-12	Sequence 12, Appl
37	1763	99.2	478	10	US-09-948-429B-8	Sequence 8, Appl
38	1763	99.2	478	12	US-10-124-807-8	Sequence 8, Appl
39	1763	99.2	478	12	US-10-291-532-8	Sequence 8, Appl
40	1763	99.2	478	14	US-10-124-305-8	Sequence 8, Appl
41	1762	99.1	729	10	US-09-825-012-52	Sequence 52, Appl
42	1762	99.1	739	10	US-09-825-012-61	Sequence 61, Appl
43	1761	99.0	330	12	US-10-159-006-22	Sequence 22, Appl
44	1761	99.0	330	15	US-10-121-454-20	Sequence 20, Appl
45	1761	99.0	451	9	US-09-920-171-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-990-586-98
; Sequence 98, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 332
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-990-586-98

Query Match 100.0%; Score 1778; DB 11; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.6e-138;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EFASKTGFVPLAPSSKSTSGGTAALGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ 60
DB 1 EFASKTGFVPLAPSSKSTSGGTAALGCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQ 60
QY 61 SSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 120
DB 61 SSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPELL 120
QY 121 GGSRVFLPPKPKDITLMISTPEVTCVVDVSHDEDEVEKFNWTVVDGVVEVHNATKPREEQ 180
DB 121 GGSRVFLPPKPKDITLMISTPEVTCVVDVSHDEDEVEKFNWTVVDGVVEVHNATKPREEQ 180

QY 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
Db 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
QY 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332
Db 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332

RESULT 2

US-10-310-113-167
; Sequence 167, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 167
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-167

Query Match 100.0%; Score 1778; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.6e-138;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EFASKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
Db 1 EFASKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
QY 61 SSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELL 120
Db 61 SSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELL 120
QY 121 GGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
Db 121 GGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
QY 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
Db 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
QY 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332
Db 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332

RESULT 3

US-10-230-880-98
; Sequence 98, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 98
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-98

Query Match 100.0%; Score 1778; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.6e-138;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EFASKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
Db 1 EFASKGPSVFFPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
QY 61 SSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELL 120
Db 61 SSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPCPAPELL 120
QY 121 GGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
Db 121 GGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
QY 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
Db 181 YNSTYRVSVLTCLVHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 240
QY 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
Db 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKS 300
QY 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332
Db 301 RMOQGNVFCSCVMHEALHNYTKQSLSPGK 332

RESULT 4

US-09-995-898A-15
; Sequence 15, Application US/0995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253Alak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50

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/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match
Best Local Similarity 99.4%; Score 1767; DB 11; Length 330;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 122
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 300
QY 303 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 332
Db 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 5
US-09-892-949-38
/ Sequence 38, Application US/09892949
/ Publication No. US2003009633A1
/ GENERAL INFORMATION:
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Gao, Zeren
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Kuijper, Joseph L.
/ APPLICANT: Maurer, Mark F.
/ TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
/ FILE REFERENCE: 00-42
/ CURRENT APPLICATION NUMBER: US/09/892,949
/ CURRENT FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: US 60/214,282
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: US 60/214,955
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 60/267,963
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 93
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 38
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-892-949-38

Query Match
Best Local Similarity 99.4%; Score 1767; DB 11; Length 330;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 122
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 300
QY 303 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 332
Db 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 6
US-10-112-582-1
/ Sequence 1, Application US/10112582
/ Publication No. US20030166877A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
/ FILE REFERENCE: LEX-017
/ CURRENT APPLICATION NUMBER: US/10/112,582
/ CURRENT FILING DATE: 2002-03-29
/ PRIOR APPLICATION NUMBER: US 60/280,625
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 330
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match
Best Local Similarity 99.4%; Score 1767; DB 12; Length 330;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 122
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 240
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSGFFLYSKLTVDKSRW 300
QY 303 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 332
Db 301 QGQNVFSCSVNHEALHNHYTQKSLSLSPGK 330
```

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RESULT 7
US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8
Query Match          99.4%; Score 1767; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120

QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180

QY 183 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 181 STYRVSVLTVLQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300

QY 303 QQGNVFSCSVNMEALHNHYTQKSLSLSPGK 332
Db 301 QQGNVFSCSVNMEALHNHYTQKSLSLSPGK 330

RESULT 9
US-10-047-542-20
; Sequence 20, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20
Query Match          99.4%; Score 1767; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASYKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 122
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCPCPAPPELLGG 120

QY 123 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 180
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QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 242
 DB 191 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 303 QCGNVFSCSVMEALHNHYTKQSLSPGK 332
 DB 301 QCGNVFSCSVMEALHNHYTKQSLSPGK 330

RESULT 10
 US-10-269-805-68
 ; Sequence 68, Application US/10269805
 ; Publication No. US20030124129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLINER, JONATHAN D.
 ; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
 ; FILE REFERENCE: A-722
 ; CURRENT APPLICATION NUMBER: US/10/269,805
 ; PRIOR FILING DATE: 2002-10-10
 ; PRIOR APPLICATION NUMBER: US 60/328,604
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 68
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-269-805-68

Query Match 99.4%; Score 1767; DB 15; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.3e-137;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVWTVPPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGG 122
 DB 61 GLYSLSVWTVPPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGG 120
 QY 123 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 DB 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 242
 DB 181 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 240
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
 QY 303 QCGNVFSCSVMEALHNHYTKQSLSPGK 332
 DB 301 QCGNVFSCSVMEALHNHYTKQSLSPGK 330

RESULT 11
 US-10-097-044A-7
 ; Sequence 7, Application US/10097044A
 ; Publication No. US20030143220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Capon, Daniel J.
 ; Gregory, Timothy J.
 ; TITLE OF INVENTION: Adhesion Variants
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/097,044A
 FILING DATE: 28-May-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,918
 FILING DATE: 1-JUN-1995
 APPLICATION NUMBER: 08/236311
 FILING DATE: 02-MAY-1994
 APPLICATION NUMBER: 07/936190
 FILING DATE: 26-AUG-1992
 APPLICATION NUMBER: 07/842777
 FILING DATE: 18-FEB-1992
 APPLICATION NUMBER: 07/250785
 FILING DATE: 28-SEP-1988
 APPLICATION NUMBER: 07/104329
 FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0444P1C3

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 371 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-097-044A-7

Query Match 99.4%; Score 1767; DB 12; Length 371;
 Best Local Similarity 100.0%; Pred. No. 6.2e-137;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 42 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101
 QY 63 GLYSLSVWTVPPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGG 122
 DB 102 GLYSLSVWTVPPSSSLGTQYICNVNHPKSTNTKVDKVEPKSCDKTHCTCPCPAPPELLGG 161
 QY 123 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 DB 162 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
 QY 183 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 242
 DB 222 STYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 281
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
 DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 341
 QY 303 QCGNVFSCSVMEALHNHYTKQSLSPGK 332
 DB 342 QCGNVFSCSVMEALHNHYTKQSLSPGK 371

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RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6
Query Match          99.4%; Score 1767; DB 15; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.8e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 115 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 174
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 122
Db 175 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 234
QY 123 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 182
Db 235 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 294
QY 183 STYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 295 STYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 354
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 355 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 414
QY 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
Db 415 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444

RESULT 13
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79
Query Match          99.4%; Score 1767; DB 12; Length 445;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 116 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 175
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 122
Db 176 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 235
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QY 183 STYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
Db 296 STYRVVSVLTVQLHQLDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 355
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 302
Db 356 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRW 415
QY 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
Db 416 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 445

RESULT 14
US-09-256-156-1
; Sequence 1, Application US/09256156A
; Publication No. US20030105294A1
; GENERAL INFORMATION:
; APPLICANT: GULLIES, Stephen D
; APPLICANT: LO, Kin-Ming
; APPLICANT: WESOLOWSKI, John
; TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
; TITLE OF INVENTION: Fusion Proteins
; FILE REFERENCE: LEX-003
; CURRENT APPLICATION NUMBER: US/09/256,156A
; CURRENT FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: US 60/075,887
; EARLIER FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: IGG-1 CHAIN C REGION
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(117)
; OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved
; OTHER INFORMATION: amino acids
US-09-256-156-1
Query Match          99.4%; Score 1767; DB 11; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 118 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 122
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Job time : 54.062 secs

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Db 238 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 297
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Db 358 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 417
Qy 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
Db 418 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 447
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RESULT 15

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US-09-822-698A-26
; Sequence 26, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hooogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822.698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 26
; LENGTH: 451
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PHI-IgG1
US-09-822-698A-26
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Query Match 99.4%; Score 1767; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 8e-137;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 122 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 181
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Qy 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 182
Db 242 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 301
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Db 302 STYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 361
Qy 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
Db 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 421
Qy 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
Db 422 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
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Search completed: January 13, 2004, 13:13:45

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 28.7057 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-98

Perfect score: 1778

Sequence: 1 EFASKGPSVFLAPSSKST.....MHEALHNHYTKSLSPGK 332

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1767	99.4	371	1	US-08-236-311-7
2	1767	99.4	371	3	US-08-457-918-7
3	1767	99.4	446	3	US-08-397-411-7
4	1767	99.4	449	1	US-08-458-516-13
5	1767	99.4	476	2	US-08-378-939-10
6	1767	99.4	951	4	US-09-313-342-9
7	1763	99.2	462	4	US-09-289-942A-7
8	1763	99.2	475	4	US-09-740-002-27
9	1763	99.2	476	3	US-08-487-550-4
10	1763	99.2	476	3	US-08-487-550-12
11	1763	99.2	476	4	US-09-526-098-4
12	1763	99.2	476	3	US-09-526-098-12
13	1763	99.2	478	3	US-08-487-550-8
14	1763	99.2	478	4	US-09-526-098-8
15	1762	99.1	459	1	US-08-157-101A-7
16	1761	99.0	330	4	US-09-301-593-22
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18	1761	99.0	451	2	US-08-887-352B-16
19	1761	99.0	451	2	US-08-887-352B-18
20	1761	99.0	451	3	US-08-466-151-65
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23	1761	99.0	451	3	US-09-109-207C-18
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26	1761	99.0	451	3	US-09-296-005-14
27	1761	99.0	451	3	US-09-296-005-16

28	1761	99.0	451	3	US-09-296-005-18
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34	1761	99.0	452	4	US-09-234-340A-71
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36	1761	99.0	454	3	US-07-934-373C-22
37	1761	99.0	454	3	US-08-437-642B-22
38	1761	99.0	454	4	US-08-146-206C-22
39	1761	99.0	454	5	PCT-US93-07832-22
40	1761	99.0	467	3	US-09-949-672A-8
41	1759	98.9	475	4	US-09-740-002-25
42	1758	98.9	472	4	US-09-301-593-30
43	1758	98.9	472	4	US-09-301-593-43
44	1758	98.9	473	3	US-09-049-672A-4
45	1756	98.8	449	4	US-09-679-397-2

ALIGNMENTS

RESULT 1
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5585335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
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Sequence 22, Appl
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Sequence 8, Appl
Sequence 25, Appl
Sequence 30, Appl
Sequence 43, Appl
Sequence 4, Appl
Sequence 2, Appl

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US-08-236-311-7
Query Match          99.4%; Score 1767; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 2e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 122
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DB 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 281
QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
DB 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 341
QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
DB 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kudinec, Jeffrey S.

US-08-457-918-7
Query Match          99.4%; Score 1767; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 2e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 42 ASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYDPEPVTVSWNSGALTSGVHTFPAVLQSS 101
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 122
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCCPCPAPELLGG 161
QY 123 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 162 PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 183 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242
DB 222 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 281
QY 243 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 302
DB 282 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 341
QY 303 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 332
DB 342 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 371

RESULT 3
US-08-397-411-7
; Sequence 7, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-7

Query Match          99.4%; Score 1767; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 2.6e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
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QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
DB 297 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 356
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLVTDKSRW 302
DB 357 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLVTDKSRW 416
QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
DB 417 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 446

RESULT 4
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GP11B/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/059,159

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match          99.4%; Score 1767; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.6e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 120 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
QY 63 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKXVEPKSCDKHTCCPPCPAPPELLGG 122
DB 180 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKXVEPKSCDKHTCCPPCPAPPELLGG 239
QY 123 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 182
DB 240 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 299
QY 183 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 242
DB 300 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 359
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLVTDKSRW 302
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLVTDKSRW 419
QY 303 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 332
DB 420 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449

RESULT 5
US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/952640
```

```
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-378-339-10

Query Match          99.4%; Score 1767; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2,9e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 147 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
QY 63 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 122
DB 207 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 266
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 267 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242
DB 327 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 446
QY 303 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 332
DB 447 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 6
US-09-313-942-9
; Sequence 9, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 951
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-9

Query Match          99.4%; Score 1767; DB 4; Length 951;
Best Local Similarity 100.0%; Pred. No. 8,2e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62

; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-378-339-10

Query Match          99.4%; Score 1767; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 2,9e-160;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 147 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
QY 63 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 122
DB 207 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 266
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 267 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 326
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242
DB 327 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 446
QY 303 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 332
DB 447 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 7
US-09-289-942A-7
; Sequence 7, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPI TOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; FILE REFERENCE: 1038-926 M15:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-289-942A-7

Query Match          99.2%; Score 1763; DB 4; Length 462;
Best Local Similarity 99.7%; Pred. No. 6,7e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 133 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 192
QY 63 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 122
DB 193 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG 252
QY 123 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
DB 253 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 312
QY 183 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 242
DB 313 STYRVSVLTIVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 372
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
DB 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 432
QY 303 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 332
DB 433 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 462
```

RESULT 8
US-09-740-002-27
; Sequence 27, Application US/09740002
; Patent No. 6537809
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; PRIOR FILING DATE: 2000-12-20
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 27
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-27

Query Match 99.2%; Score 1763; DB 4; Length 475;
Best Local Similarity 99.7%; Pred. No. 6.9e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPFPVTVSNWNGALTSVHTFPVAVLQSS 62
DB 146 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPFPVTVSNWNGALTSVHTFPVAVLQSS 205
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 122
DB 206 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 265
QY 123 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 182
DB 266 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 325
QY 183 STYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 242
DB 326 STYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 385
QY 243 LTKQVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
DB 386 LTKQVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 445
QY 303 QQGNVFCSCVMHEALHNYTKSLSPGK 332
DB 446 QQGNVFCSCVMHEALHNYTKSLSPGK 475

RESULT 9
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA

ZIP: 22314
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-4

Query Match 99.2%; Score 1763; DB 3; Length 476;
Best Local Similarity 99.7%; Pred. No. 7e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPFPVTVSNWNGALTSVHTFPVAVLQSS 62
DB 147 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVDFPFPVTVSNWNGALTSVHTFPVAVLQSS 206
QY 63 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 122
DB 207 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 266
QY 123 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 182
DB 267 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNAKTKPREEQYN 326
QY 183 STYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 242
DB 327 STYRVVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 386
QY 243 LTKQVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 302
DB 387 LTKQVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 446
QY 303 QQGNVFCSCVMHEALHNYTKSLSPGK 332
DB 447 QQGNVFCSCVMHEALHNYTKSLSPGK 476

RESULT 10
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/487,550
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-12

Query Match 99.2%; Score 1763; DB 3; Length 476;
Best Local Similarity 99.7%; Pred. No. 7e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 62
DB 147 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 206
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLGG 122
DB 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKAEPKSCDKHTCTCPAPPELLGG 266
QY 123 PSVELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 182
DB 267 PSVELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 326
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446
QY 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332
DB 447 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 11

US-09-526-098-4

Sequence 4, Application US/09526098

Patent No. 6492134

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/526,098
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-4

Query Match 99.2%; Score 1763; DB 4; Length 476;
Best Local Similarity 99.7%; Pred. No. 7e-160;
Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 62
DB 147 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 206
QY 63 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCTCPAPPELLGG 122
DB 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKAEPKSCDKHTCTCPAPPELLGG 266
QY 123 PSVELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 182
DB 267 PSVELFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPREEQYN 326
QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
DB 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 302
DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 446
QY 303 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 332
DB 447 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 12

US-09-526-098-12

Sequence 12, Application US/09526098

Patent No. 6492134

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

IMMUNOSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/526,098
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/383,916
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 476 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-526-098-12

Query Match 99.2%; Score 1763; DB 4; Length 476;
 Best Local Similarity 99.7%; Pred. No. 7e-160;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 Db 147 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206
 QY 63 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTPCPAPPELLGG 122
 Db 207 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHCTPCPAPPELLGG 266
 QY 123 PSVFLFPKPKDILMI SRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 182
 Db 267 PSVFLFPKPKDILMI SRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 326
 QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 Db 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 386
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
 Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 446
 QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332
 Db 447 QQGNVFCSCVMHEALHNYTKQSLSPGK 476

RESULT 13
 ; US-08-487-550-8
 ; Sequence 8, Application US/08487550
 ; Patent No. 6113898
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Darrell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria

; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,550
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 478 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-487-550-8

Query Match 99.2%; Score 1763; DB 3; Length 478;
 Best Local Similarity 99.7%; Pred. No. 7e-160;
 Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 Db 149 ASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 208
 QY 63 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHCTPCPAPPELLGG 122
 Db 209 GLYSLSVVTVFPSSSLGTQYICNVNHPKNTKVDKKAEPKSCDKTHCTPCPAPPELLGG 268
 QY 123 PSVFLFPKPKDILMI SRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 182
 Db 269 PSVFLFPKPKDILMI SRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 328
 QY 183 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
 Db 329 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 388
 QY 243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 302
 Db 389 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 448
 QY 303 QQGNVFCSCVMHEALHNYTKQSLSPGK 332
 Db 449 QQGNVFCSCVMHEALHNYTKQSLSPGK 478

RESULT 14
 ; US-09-526-098-8
 ; Sequence 8, Application US/09526098
 ; Patent No. 6492134
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Darrell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA

; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/526,098
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/383,916
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 478 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-526-098-8

Query Match 99.2%; Score 1763; DB 4; Length 478;

Best Local Similarity 99.7%; Pred. No. 7e-160; Mismatches 0; Indels 0; Gaps 0;

Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3	ASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	62
Db	149	ASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	208
QY	63	GLYSLSVVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKHTCCPPCPAPPELLGG	122
Db	209	GLYSLSVVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKHTCCPPCPAPPELLGG	268
QY	123	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	182
Db	269	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	328
QY	183	STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	242
Db	329	STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	388
QY	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	302
Db	389	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	448
QY	303	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	332
Db	449	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	478

RESULT 15

US-08-157-101A-7

; Sequence 7, Application US/08157101A

; Patent No. 5808032

; GENERAL INFORMATION:

; APPLICANT: KURIHARA, TATSUYA

; APPLICANT: MATSUKURA, SHIGEKAZU

; APPLICANT: TSURUOKA, NOBUO

; APPLICANT: ARIMA, KENJI

; APPLICANT: NISHIHARA, TATSURO

; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION

; TITLE OF INVENTION: PLASMIDS THEREFOR

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/157,101A
 ; FILING DATE: 05-APR-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: TITUS, MARLANA K
 ; REGISTRATION NUMBER: 35843
 ; REFERENCE/DOCKET NUMBER: 9437/204199
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3711
 ; TELEFAX: 202-822-0944
 ; TELEX: 6714627 CUCH
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 459 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-157-101A-7

Query Match 99.1%; Score 1762; DB 1; Length 459;

Best Local Similarity 99.7%; Pred. No. 8.2e-160; Mismatches 1; Indels 0; Gaps 0;

Matches 329; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3	ASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	62
Db	130	ASTKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS	189
QY	63	GLYSLSVVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKHTCCPPCPAPPELLGG	122
Db	190	GLYSLSVVTVPSSSLGTQYICNVNHPKSNKTKVDKVPKSCDKHTCCPPCPAPPELLGG	249
QY	123	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	182
Db	250	PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	309
QY	183	STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	242
Db	310	STYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPRFPQVYTLPPSRDE	369
QY	243	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	302
Db	370	LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW	429
QY	303	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	332
Db	430	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	459

Search completed: January 13, 2004, 12:46:35

Job time : 30.7057 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 ; Search time 7.75633 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFIIPPSPDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	215	2 JE0244	Ig kappa chain NIG
2	553	100.0	215	2 JE0242	Ig kappa chain NIG
3	553	100.0	215	2 JE0243	Ig kappa chain NIG
4	550	99.5	135	2 S52059	JC-kappa protein -
5	548	99.1	106	1 K3HU	Ig kappa chain C r
6	537	97.1	216	2 JE0241	Ig kappa chain Am3
7	520	94.0	215	2 A23746	Ig kappa chain V-I
8	513	92.8	99	2 A37927	Ig kappa chain C r
9	507	91.7	99	2 S26653	Ig kappa chain C r
10	372	67.3	240	2 S06084	Ig kappa chain pre
11	367	66.4	106	1 KIRB	Ig kappa chain C r
12	366	66.2	178	2 PT0219	Ig kappa chain C r
13	359	64.9	106	1 KIRTA	Ig kappa chain C r
14	358	64.7	217	2 S42772	Ig kappa chain - m
15	358	64.7	218	2 S68241	Ig kappa chain V r
16	358	64.7	219	2 S38865	Ig kappa chain - m
17	352	63.7	218	2 JC5810	nonoclonal antibod
18	352	63.7	219	2 PC4203	Ig kappa chain (mo
19	352	63.7	219	2 S16112	Ig kappa chain V r
20	352	63.7	219	2 S52028	Ig kappa chain - m
21	352	63.7	220	2 A31790	Ig kappa chain V r
22	352	63.7	225	2 S37484	Ig kappa chain - m
23	352	63.7	234	2 S14237	Ig kappa chain pre
24	352	63.7	234	2 S01320	Ig kappa chain pre
25	352	63.7	235	2 S25058	Ig kappa chain - m
26	350	63.3	106	1 KIMS	Ig kappa chain C r
27	350	63.3	126	2 I54782	gene Pvt-1a/Ig-Ck
28	348	62.9	225	2 JL0029	Ig kappa chain pre
29	345	62.4	230	2 S33161	Ig kappa chain - s

30	321	58.0	214	2 S68212	Ig kappa chain (Wa
31	312	56.4	210	2 A56169	Ig kappa chain V r
32	308.5	55.8	106	2 G20907	Ig kappa-B4 chain
33	306.5	55.4	106	1 K4RBBS	Ig kappa-2 chain C
34	277.5	50.2	229	2 A20969	Ig kappa chain pre
35	257.5	46.6	103	1 K4RB	Ig kappa-B4 chain
36	256	46.3	104	2 F53275	Ig kappa-1 chain C
37	246.5	44.6	104	1 K9RB	Ig kappa-B9 chain
38	245	44.3	238	2 A49633	Ig lambda-like cha
39	241	43.6	104	1 K5RBV	Ig kappa chain C r
40	237	42.9	118	2 A46518	Ig L1 chain J-C re
41	231	41.8	103	2 B26167	Ig lambda chain C
42	231	41.8	213	2 A21177	Ig light chain pre
43	225	40.7	108	1 K3PG	Ig light chain C r
44	223.5	40.4	103	1 K5RB	Ig kappa-B5 chain
45	222	40.1	197	2 S29593	Ig kappa chain (W)

ALIGNMENTS

RESULT 1

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 553; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 2.6e-47;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60

109 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 168

DB

61 SKDSTYSLSSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRGEC 107

169 SKDSTYSLSSTLTLSKADYERKHYACEVTHQGLSSPVTKSFNRGEC 215

DB

RESULT 2

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

QY

1 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60

109 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 168

DB

109 RTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQSVTEQD 168

DB

QY 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||
 Db 169 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
 |||
 RESULT 3
 JEO243
 Ig kappa chain NIG93 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C/Accession: JEO243
 R/Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
 A:Reference number: JEO243
 A:Accession: JEO243
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMV>
 Query Match 100.0%; Score 553; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 2.6e-47;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 |||
 Db 109 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168
 |||
 QY 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||
 Db 169 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215
 |||
 RESULT 4
 S52059
 JC-kappa protein - human
 C:Species: Homo sapiens (man)
 C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
 C/Accession: S52059
 R/Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S.;
 EMBO J. 13, 5937-5943, 1994
 A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy c
 A:Reference number: S52059; MUID:95112804; PMID:7813432
 A:Accession: S52059
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <FRA>
 C:Superfamily: pre-B cell omega light chain; immunoglobulin homology
 Query Match 99.5%; Score 550; DB 2; Length 135;
 Best Local Similarity 99.1%; Pred. No. 2.9e-47;
 Matches 106; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 |||
 Db 29 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 88
 |||
 QY 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||
 Db 89 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 135
 |||
 RESULT 5
 K3HU
 Ig kappa chain C region - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1980 #sequence_revision 02-Jul-1998 #text_change 21-Jul-2000
 C/Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
 R/Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
 Biochemistry 9, 3153-3161, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequenc

A:Reference number: A90562; MUID:71064023; PMID:5489770
 A:Contents: myeloma protein Eu
 A:Accession: B90562
 A:Molecule type: protein
 A:Residues: 1-106 <GOT>
 A>Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
 R/Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
 A:Reference number: A90565; MUID:71064027; PMID:4923144
 A:Contents: annotation; Eu, disulfide bonds
 R/Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
 A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sul
 A:Reference number: A91651; MUID:72188439; PMID:5027703
 A:Contents: Bence Jones protein Ti
 A:Accession: A91651
 A:Molecule type: protein
 A:Residues: 1-106 <SUT>
 R/Hietter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
 Cell 22, 197-207, 1980
 A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserv
 A:Reference number: A90806; MUID:81042304; PMID:6775818
 A:Accession: A90806
 A:Molecule type: DNA
 A:Residues: 1-106 <HIE>
 A:Cross-references: GB:J00241; NID:933140; PIDN:CAA23823.1; PID:gl335148
 A>Note: the sequence was determined from the germline gene
 R/Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,
 in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
 A:Reference number: A94417
 A:Contents: Bence Jones protein Roy
 A:Accession: A94417
 A:Molecule type: protein
 A:Residues: 1-44, A', 46-56, Q', 58-82, L', 84-106 <HIL>
 A>Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and 83-Leu
 R/Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
 A:Title: Die vollständige Aminosäuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ).
 A:Reference number: A91639; MUID:68242259; PMID:5586923
 A:Contents: Bence Jones protein Cum
 A:Accession: A91639
 A:Molecule type: protein
 A:Residues: 1-56, Q', 58-106 <H12>
 R/Titani, K.; Shinoda, T.; Putnam, F.W.
 J. Biol. Chem. 244, 3550-3560, 1969
 A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete
 A:Reference number: A92047; MUID:69234734; PMID:4893882
 A:Contents: Bence Jones protein Ag
 A:Accession: A92047
 A:Molecule type: protein
 A:Residues: 1-13, N', 15-106 <TIT>
 R/Köhler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.
 Science 169, 56-59, 1970
 A:Title: Macroglobulin structure: variable sequence of light and heavy chains.
 A:Reference number: A94242; MUID:70201507; PMID:5447531
 A:Contents: Waldenström's macroglobulin Ou
 A:Accession: A94242
 A:Molecule type: protein
 A:Residues: 1-13, N', 15-106 <KOH>
 R/Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
 Am. J. Hum. Genet. 48, 613-620, 1991
 A:Title: Km typing with PCR: application to population screening.
 A:Reference number: A37927; MUID:91150772; PMID:1900145
 A:Accession: B37927
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 8-106 <KUR>
 A>Note: allotype Inv(3)
 R/Steiner, V.; Chang, J.Y.
 FEBS Lett. 22, 6-10, 1987
 A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
 A:Reference number: S02572; MUID:88005152; PMID:3115831

A:Contents: annotation
 C:Genetics:
 A:Gene: GDB:IGKC
 A:Cross-references: GDB:120088; OMIM:147200
 A:Map position: 2p12-2p12
 C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds; in some cases, such as IGA and IGM, the subunits associate into 1a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:19-88/Domain: immunoglobulin homology <IMM>
 F:26-86/Disulfide bonds: #status experimental
 F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 99.1%; Score 549; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 3.4e-47;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61
 Db 1 TVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 6
 JB0241
 Ig kappa chain Am37 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: J02041
 R:Alim, M.A.; Yamaki, S.; Hoesain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
 Submitted to JIPID, November 1998
 A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
 A:Reference number: JB0241
 A:Accession: J02041
 A:Molecule type: protein
 A:Residues: 1-216 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 97.1%; Score 537; DB 2; Length 216;
 Best Local Similarity 97.2%; Pred. No. 9.9e-46;
 Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RTVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 110 RTVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 170 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 7
 A23746
 Ig kappa chain V-III (KAU cold agglutinin) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
 C:Accession: A23746
 R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
 J. Biol. Chem. 266, 2836-2842, 1991
 A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
 A:Reference number: A23746; MUID:91131575; PMID:1993660
 A:Accession: A23746
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-215 <LEO>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 94.0%; Score 520; DB 2; Length 215;
 Best Local Similarity 98.1%; Pred. No. 4.7e-44;
 Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 109 RTVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

QY 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106
 Db 169 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8
 A37927
 Ig kappa chain C region (allotype Inv(1.2)) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
 C:Accession: A37927
 R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.
 Am. J. Hum. Genet. 48, 613-620, 1991
 A:Title: Km typing with PCR: application to population screening.
 A:Reference number: A37927; MUID:91150772; PMID:1900145
 A:Accession: A37927
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-99 <KUR>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 92.8%; Score 513; DB 2; Length 99;
 Best Local Similarity 99.0%; Pred. No. 9e-44;
 Matches 98; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 FIPPPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 68
 Db 1 FIPPPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 60

QY 69 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Db 61 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 99

RESULT 9
 S26653
 Ig kappa chain C region - chimpanzee (fragment)
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
 C:Accession: S26653
 R:Enrich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
 Hum. Antibodies Hybridomas 1, 23-26, 1990
 A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
 A:Reference number: S26652; MUID:91355693; PMID:2129418
 A:Accession: S26653
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-99 <EHR>
 A:Cross-references: EMBL:X65287
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 91.7%; Score 507; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 3.5e-43;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61
 Db 1 TVAAPSVPFPPSPDQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 62 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 100

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Db 61 KDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTK 99
RESULT 10
IG kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CR>
A:CROSS-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: IG kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>
Query Match 67.3%; Score 372; DB 2; Length 240;
Best Local Similarity 65.4%; Pred. No. 2.3e-29;
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGNSQESVTEQD 60
Db 134 RADAAPTVSIIPPSTEQLATGASVCLMNNFYPRDISVKWKIDGTERRDGVLDSTVDQD 193
QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 194 SKDSTYSNSSLTLSLKADYSHNLYTCEVVKHTSSSPVVKSFNRNEC 240
RESULT 11
KIRTB
IG kappa chain C region (allele b) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 28-May-1999
C:Accession: A93901; MUID:82082587; PMID:6273908
R:Sheppard, H.W.; Gutman, G.A.
Proc.Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the le
A:Reference number: A93901; MUID:82082587; PMID:6273908
A:Accession: A93901
A:Molecule type: DNA
A:Residues: 1-106 <SHE>
A:CROSS-references: GB:V01241; GB:J00745; GB:J02574; GB:J02575; NID:G57849; PIDN:CAA2455
A:Experimental source: strain LOU
R:Starace, V.; Querinjean, P.
J. Immunol. 115, 59-62, 1975
A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation
A:Reference number: A92807; MUID:75212238; PMID:807630
A:Contents: Bence Jones protein S211
A:Accession: A92807
A:Molecule type: Protein
A:Residues: 1, 'N', 'J', '3-29', 'K', '31-47, 49-78, 'Q', '80-86, 'Q', '88-98, 'W', '99, 'N', '101-106 <STA>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer
F:19-88/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status predicted
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 66.4%; Score 367; DB 1; Length 106;
Best Local Similarity 65.4%; Pred. No. 2.5e-29;
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 4 AAPSVPFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGNSQESVTEQD 63
Db 61 KDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTK 99
RESULT 12
PT0219
IG kappa chain V-C region (PLC18) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: PT0219
R:Lammers, B.M.; Beaman, K.D.; Kim, Y.B.
Mol. Immunol. 28, 877-880, 1991
A:Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.
A:Reference number: PT0219; MUID:91342694; PMID:1715030
A:Accession: PT0219
A:Molecule type: mRNA
A:Residues: 1-178 <LAM>
A:CROSS-references: GB:M59321; NID:G164508; PIDN:AAA03520.1; PID:G164509
A:Experimental source: spleen, strain Minnesota Miniature
A:Note: the authors translated the codon CTC for residue 141 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-70/Domain: V region (fragment) <VRG>
F:12-18/Region: complementarity-determining 1
F:19-51/Region: framework 1
F:52-60/Region: complementarity-determining 2
F:61-70/Region: framework 2
F:71-178/Domain: C region <CRG>
F:96-156/Disulfide bonds: #status predicted
F:176/Disulfide bonds: interchain #status predicted
Query Match 66.2%; Score 366; DB 2; Length 178;
Best Local Similarity 64.5%; Pred. No. 6.1e-29;
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAKVQWKVDNALQSGNSQESVTEQD 60
Db 70 RADAXPSVFIIPFPEKEQLATPTVSVCLINNFFPREISVKWKVGVQVSSGHPDPSVTEQD 129
QY 61 SKDSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 130 SKDSTYSLSTLTLSPTSOYLSHNLYSCVTHKTLASPLVTSFNRNEC 176
RESULT 13
KIRTA
IG kappa chain C region (allele a) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 22-Jun-1999
C:Accession: A02118
R:Sheppard, H.W.; Gutman, G.A.
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981
A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the l
A:Reference number: A93901; MUID:82082587; PMID:6273908
A:Accession: A02118
A:Molecule type: DNA
A:Residues: 1-106 <SHE>
A:CROSS-references: GB:J02574; GB:J00745; NID:G204820; PIDN:AAA4141.1; PID:G204821
A:Experimental source: strain DA
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer
F:19-88/Domain: immunoglobulin homology <IMM>
F:26-86/Disulfide bonds: #status predicted
F:106/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 64.9%; Score 359; DB 1; Length 106;
Best Local Similarity 63.5%; Pred. No. 1.6e-28;
Matches 66; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
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Search completed: January 13, 2004, 12:44:42
Job time : 7.75633 secs

S42772

RESULT 15

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 4.67249 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFFPPSDQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	99.1	106	1 KAC_HUMAN	P01834 homo sapien
2	367	66.4	106	1 KAC_RAT	P01835 rattus norv
3	359	64.9	106	1 KAC_RAT	P01836 rattus norv
4	350	63.3	106	1 KAC_MOUSE	P01837 mus musculu
5	306.5	55.4	106	1 KAC_RABIT	P01839 oryctolagus
6	257.5	46.6	103	1 KAC9_RABIT	P01840 oryctolagus
7	246.5	44.6	104	1 KAC6_RABIT	P01838 oryctolagus
8	241	43.6	104	1 KAC6_RABIT	P01840 oryctolagus
9	231	41.8	103	1 LAC_CHICK	P03984 oryctolagus
10	225	40.7	108	1 KAC_RANCA	P20763 gallus gall
11	223.5	40.4	103	1 KAC_RABIT	P11272 rana catesb
12	210.5	38.1	105	1 LAC1_MOUSE	P01841 oryctolagus
13	208.5	37.7	105	1 LAC1_MOUSE	P01843 mus musculu
14	203.5	36.8	105	1 LAC_HUMAN	P01842 homo sapien
15	190	34.4	104	1 LAC_RABIT	P01847 oryctolagus
16	187.5	33.9	213	1 ILLI_HUMAN	P20766 rattus norv
17	183	33.1	104	1 LAC2_RAT	P15814 homo sapien
18	180.5	32.6	105	1 LAC2_RAT	P20767 rattus norv
19	178	32.2	104	1 LAC3_MOUSE	P01846 sus scrofa
20	174	31.5	104	1 LAC2_MOUSE	P01845 mus musculu
21	164.5	29.7	329	1 GC2_CAVPO	P01844 mus musculu
22	161.5	29.2	105	1 LAC5_MOUSE	P01862 cavia porce
23	157.5	28.5	421	1 EPC_MOUSE	P20765 mus musculu
24	153.5	27.8	330	1 GCAN_MOUSE	P01863 mus musculu
25	153.5	27.8	339	1 GCAN_MOUSE	P01863 mus musculu
26	151	27.3	326	1 GC2_HUMAN	P01865 mus musculu
27	151	27.3	327	1 GC4_HUMAN	P01859 homo sapien
28	150.5	27.2	335	1 GCAB_MOUSE	P01861 homo sapien
29	149	26.9	290	1 GC1_HUMAN	P01864 mus musculu
30	148	26.8	330	1 GC1_HUMAN	P01860 homo sapien
31	146.5	26.5	105	1 LAC5_MOUSE	P01857 homo sapien
32	145	26.2	336	1 LAC5_MOUSE	P20764 mus musculu
33	145	26.2	405	1 GCEN_MOUSE	P01866 mus musculu
					P01867 mus musculu

34	143.5	25.9	323	1 GC_RABIT	P01870 oryctolagus
35	143	25.9	454	1 MUC_MESAU	P06337 mesocricetu
36	142.5	25.8	457	1 MUC_SUNMU	P20768 suncus muri
37	141.5	25.6	429	1 EPC_RAT	P01855 rattus norv
38	137.5	24.9	329	1 GC_RAT	P20762 rattus norv
39	137	24.8	324	1 GC1_MOUSE	P01868 mus musculu
40	137	24.8	393	1 GC1_MOUSE	P01869 mus musculu
41	136	24.6	455	1 MUC_MOUSE	P01872 mus musculu
42	136	24.6	476	1 MUCM_MOUSE	P01873 mus musculu
43	135	24.4	322	1 GCA_RAT	P20760 rattus norv
44	135	24.4	329	1 GC3_MOUSE	P22436 mus musculu
45	135	24.4	398	1 GC3_MOUSE	P03987 mus musculu

ALIGNMENTS

RESULT 1
KAC_HUMAN
ID_ KAC_HUMAN STANDARD; PRT; 106 AA.
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain C region.
GN IGKC.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN EU).
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RL Intrachain disulfide bonds.";
RN [3]
RP Biochemistry 9:3188-3196(1970).
RX SEQUENCE (BENCE-JONES PROTEIN TI).
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The complete amino acid sequence and its significance for
the mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=81042304; PubMed=6775818;
RA Hieber P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT "Cloned human and mouse kappa immunoglobulin constant and J region
genes conserve homology in functional segments.";
RN [5]
RP Cell 22:197-207(1980).
RX SEQUENCE (BENCE-JONES PROTEIN ROY).
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
RN [6]
RP SEQUENCE (BENCE-JONES PROTEIN CUM).
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RX TISSUE=Abdominal adipose tissue;
RA Olsen K.E., Sletten K., Westermarck P.;
RT subcutaneous fat biopsy; kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; J00241; AAA58989.1; --
DR ENBL; V00557; CAA23823.1; --
DR PIR; B90562; K3HU.
DR PDB; 1D53; 09-FEB-00.
DR PDB; 1D51; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1HEZ; 10-AUG-01.
DR PDB; 1LKL; 12-MAR-97.
DR PDB; 1I7Z; 08-AUG-01.
DR PDB; 1MIM; 15-MAY-97.
DR Genew; HGNC:5716; IGKC.
DR MIM; 147200; --
DR GO; GO:0003823; Fc antigen binding activity; NAS.
DR GO; GO:0006955; P. immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
KW NON_TER 1 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT CONFLICT 2 2 D -> N (IN REF. 2).
FT CONFLICT 30 30 N -> K (IN REF. 2).
FT CONFLICT 48 48 MISSING (IN REF. 2).
FT CONFLICT 79 79 E -> Q (IN REF. 2).
FT CONFLICT 87 87 E -> Q (IN REF. 2).
FT CONFLICT 98 98 V -> W (IN REF. 2).
FT CONFLICT 100 100 S -> N (IN REF. 2).
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FD372CE8 CRC64;
Query Match 99.1%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.5e-48;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61

Db 1 TVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 62 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 106
RESULT 2
KACB RAT
ID KACB RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE IG kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Louvain;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes.";
RJ. Immunol. 115:59-62(1975).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93901; KIRTB.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT CONFLICT 2 2 D -> N (IN REF. 2).
FT CONFLICT 30 30 N -> K (IN REF. 2).
FT CONFLICT 48 48 MISSING (IN REF. 2).
FT CONFLICT 79 79 E -> Q (IN REF. 2).
FT CONFLICT 87 87 E -> Q (IN REF. 2).
FT CONFLICT 98 98 V -> W (IN REF. 2).
FT CONFLICT 100 100 S -> N (IN REF. 2).
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820D1CA36 CRC64;
Query Match 66.4%; Score 367; DB 1; Length 106;
Best Local Similarity 65.4%; Pred. No. 5.3e-30;
Matches 68; Conservative 14; Mismatches 22; Indels 0; Gaps 0;
QY 4 AAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK 63
Db 3 AAPTSVIFPPSDEQLKSGTASVCLNNFYPRIIDISVKKIDGTRDGLDVSVDQDSK 62
QY 64 STYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 63 STYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 106
RESULT 3

KACA_RAT
ID_KACA_RAT STANDARD; PRT; 106 AA.
AC P01836;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region, A allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RP STRAIN=DA;
RX MEDLINE=82082587; PubMed=62733908;
RA Sheppard H.W., Gutman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02118; K1RTA.
DR HSSP; P01842; 2MCG.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;

Query Match 64.98; Score 359; DB 1; Length 106;
Best Local Similarity 63.59; Pred. No. 3.3e-29;
Matches 66; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

Qy 4 AAPSFFIPPSDEQLKSGTASVVCLLNNFYPRBAKVQWKVDNALQSGNSQSVTEQDSKD 63
Db 3 AAPTFSIFPSSMEGLTSGGATVVCVNNFYPRDISVKWKIDGSEQRDGLVSDVTDQSDK 62

Qy 64 STVSLSTLTKADYKHKYKACEVTHQGLSPFTVSKFNRGEC 107
Db 63 STVSMSTLSLTKEVERHNLTYCEVVKHTSSSPVVKSFNRNEC 106

RESULT 4
KAC_MOUSE
ID_KAC_MOUSE STANDARD; PRT; 106 AA.
AC P01837;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG kappa chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE (MOPC 21).
RP MEDLINE=73053310; PubMed=4638343;
RA Svasthi J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain."
RL Biochem. J. 128:427-444(1972).
RN D-SULFIDE BONDS (MOPC 21).
RP MEDLINE=7308889; PubMed=5073237;
RA Svasthi J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RL Biochem. J. 126:837-850(1972).

RN [3]
RP SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
RX MEDLINE=79084137; PubMed=103625;
RA Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
RT "Complete sequence of constant and 3' noncoding regions of an
RT immunoglobulin mRNA using the dideoxynucleotide method of RNA
RT sequencing.";
RL Cell 15:1057-1075(1978).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RL Nucleic Acids Res. 9:4485-4494(1981).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=81191915; PubMed=6262318;
RA Max E.E., Maizel J.V. Jr., Leder P.;
RT "The nucleotide sequence of a 5.5-kilobase DNA segment containing the
RT mouse kappa immunoglobulin J and C region genes.";
RL J. Biol. Chem. 256:5116-5120(1981).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198949; PubMed=6785724;
RA Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RT kappa chain.";
RL Nucleic Acids Res. 9:971-981(1981).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RT phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
RN [8]
RP -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; V00807; CRA24189.1; -;
DR PIR; B90282; KIMS.
DR PDB; 1AIF; 01-FEB-97.
DR PDB; 1FSK; 02-OCT-00.
DR PDB; 1IGC; 03-JUN-95.
DR PDB; 1KBS; 08-APR-98.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCU; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96495; Igk-C.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11778 MW; 4B51FF5EF49ABE5 CRC64;

Query Match 63.3%; Score 350; DB 1; Length 106;
 Best Local Similarity 61.5%; Pred. No. 2.6e-28;
 Matches 64; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 4 AAPSVPFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63
 DB 3 AAPTSTLTLTKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 QY 64 STYLSSTLTLTKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 DB 63 STYMSSTLTLTKDEYERHNSYTCAHTKSTSPVKSFRNEC 106

RESULT 5
 KACB_RABIT
 ID KACB_RABIT STANDARD; PRT; 106 AA.
 AC P01839;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG kappa-B4 chain C region.
 GN K-BAS
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82060334; PubMed=6795636;
 RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
 RT "Multiplicity of constant kappa light chain genes in the rabbit
 genome: a B4b4 homozygous rabbit contains a kappa-bas gene.";
 RL EMOB J. 2:437-441(1983).
 CC -1- MISCELLANEOUS: IN BASILEA RABBITS, THE MAJOR TYPE OF LIGHT CHAIN
 IS LAMBDA. THE KAPPA CHAIN SHOWN IS A MINOR COMPONENT. ALL OTHER
 RABBIT B ALLOTYPES HAVE 64-CYS.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; V01241; CAA24558.1; -
 DR EMBL; V00885; -; NOT_ANNOTATED_CDS.
 DR PIR; A02121; K4RBBS.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 99
 FT DOMAIN 6 99 IG-LIKE.
 FT DISULFID 27 87
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 106 AA; 11279 MW; AF9B928D8A853849 CRC64;

Query Match 55.4%; Score 306.5; DB 1; Length 106;
 Best Local Similarity 54.4%; Pred. No. 5.8e-24;
 Matches 56; Conservative 16; Mismatches 30; Indels 1; Gaps 1;

QY 5 APSVTFPPSDEQLKSGTASVWCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 64
 DB 5 APSVLLFPPSKBELTGTATIVCVANKFYPSDITVTKVDGTTQSGIENSKTPQSPEDN 64
 QY 65 TYSLSSTLTLTKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

Db 65 TYSLSSTLTLTKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106
 RESULT 6
 KAC4_RABIT
 ID KAC4_RABIT STANDARD; PRT; 103 AA.
 AC P01840;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG kappa-B4 chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83300036; PubMed=6412231;
 RA Emorine L., Dreher K.L., Kindt T.J., Max E.E.;
 RT "Rabbit immunoglobulin kappa genes: structure of a germline b4
 allotype J-C locus and evidence for several b4-related sequences in
 the rabbit genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82060334; PubMed=6795636;
 RA Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.;
 RT "Nucleotide sequence of constant and 3' untranslated regions of a
 kappa immunoglobulin light chain mRNA of a homozygous b4 rabbit.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=75133568; PubMed=1091650;
 RA Chen K.C.S., Kindt T.J., Krause R.M.;
 RT "Primary structure of the L chain from a rabbit homogeneous antibody
 to streptococcal carbohydrate. II. Sequence determination of peptides
 from tryptic and peptic digests.";
 RL J. Biol. Chem. 250:3289-3296(1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE
 SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM
 THE SERUM OF A SINGLE RABBIT.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X00231; CAA25051.1; -
 DR PIR; A93971; K4RB.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1 95
 FT DOMAIN 5 95 IG-LIKE.
 FT DISULFID 26 85
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT CONFLICT 58 58 N -> D (IN REF. 3).
 SQ SEQUENCE 103 AA; 11043 MW; 5FCSACCB60E68DB CRC64;

Query Match 46.6%; Score 257.5; DB 1; Length 103;
 Best Local Similarity 48.5%; Pred. No. 4.4e-19;
 Matches 50; Conservative 21; Mismatches 29; Indels 3; Gaps 3;

QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDS 64
 DB 4 APTVLFFPAPQVAIGTIVVCVANKYFP-DVTVTWEVDGTTGTGTGKNSKTPONSADC 62
 QY 65 TYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
 DB 63 TYNLSSTLTLTSTQYNSHKEYTKVT-QGTTS-VVQSFNRGDC 103

RESULT 7

KAC9_RABIT
 ID KAC6_RABIT STANDARD; PRT; 104 AA.
 AC P01838;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG kappa-B3 chain C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76176480; PubMed=817288;
 RA Farnsworth V., Goodflesh R., Rodkey S., Hood L.;
 RT "Immunoglobulin allotypes of rabbit kappa chains: polymorphism of a
 RT control mechanism regulating closely linked duplicated genes?";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:1293-1296(1976).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM POOLED IMMUNOGLOBULIN
 CC OF HOMOCYGOUS B9 RABBITS.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02120; K9RB.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 6 100 IG-LIKE.
 FT DISULFID 27 86
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 104 AA; 11347 MW; 427B1668B0EC8D99 CRC64;

Query Match 44.6%; Score 246.5; DB 1; Length 104;
 Best Local Similarity 46.6%; Pred. No. 5.5e-18;
 Matches 48; Conservative 18; Mismatches 34; Indels 3; Gaps 3;

QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDS 64
 DB 5 APTVLFFPAPQVAIGTIVVCVANKYFP-DVTVTWEVDGTTGTGTGKNSKTPONSADC 62

QY 65 TYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
 DB 65 TYNLSSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 104

RESULT 8

KAC6_RABIT
 ID KAC6_RABIT STANDARD; PRT; 104 AA.
 AC P03984;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG kappa chain B5 variant C region.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN SEQUENCE FROM N.A. (CLONE PKB5-F2).
 RP MEDLINE=84041515; PubMed=6314281;
 RX Bernstein K.E., Skurla R.M. Jr., Mage R.G.;
 RA "The sequences of rabbit kappa light chains of b4 and b5 allotypes
 RT differ more in their constant regions than in their 3' untranslated
 RT regions.";
 RL Nucleic Acids Res. 11:7205-7214(1983).
 CC -!- MISCELLANEOUS: THE CDNA FROM WHICH THIS SEQUENCE WAS DERIVED
 CC CONTAINS A TERMINATOR CODON WITHIN THE V-REGION CODING REGION. THE
 CC ORIGIN OF THIS CODON AND OF THE DIFFERENCES BETWEEN THIS AND OTHER
 CC SEQUENCED B5 C REGIONS ARE UNCLEAR. THE CDNA CLONE WAS MADE USING
 CC MRNA FROM TRYPAANOSOME-INFECTED B5-HOMOCYGOUS RABBITS.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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EMBL; K01363; AAA31355.1; -;
 DR PIR; A02124; KSRBV.
 DR HSSP; P01842; 2MCG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00407; IGc1; 1.
 DR PROSITE; PS00835; IG-LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 5 100 IG-LIKE.
 FT DISULFID 26 85
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 104 AA; 11079 MW; 7C71850205381751 CRC64;

Query Match 43.6%; Score 241; DB 1; Length 104;
 Best Local Similarity 46.6%; Pred. No. 2e-17;
 Matches 48; Conservative 18; Mismatches 35; Indels 2; Gaps 2;

QY 5 APSVFIFPPSDQLKSGTASVVLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDS 64
 DB 4 APTVLFFPAPQVAIGTIVVCVANKYFP-DGTVTWQVDGKPLTTGTGTSKTPQNSDDC 62

QY 65 TYSLSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 107
 DB 63 TYNLSSTLTLSKADYKHKYKACVETHQGLSSPVTKSFNRGEC 104

RESULT 9

LAC_CHICK
 ID LAC_CHICK STANDARD; PRT; 103 AA.
 AC P20763;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE IG lambda chain C region.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87218480; PubMed=3107981;
 RA Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
 RT "Analyses of chicken immunoglobulin light chain cDNA clones indicate
 RT a few germline V lambda genes and allotypes of the C lambda locus.";
 RL EMBL J. 6:97-102(1987).


```

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X04768; CAA28461.1; ..
DR PIR; B26167; B26167.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1
FT DISULFID 28 85
FT DISULFID 103 103
FT VARIANT 90
FT VARIAT 90
SQ SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;
Query Match 41.8%; Score 231; DB 1; Length 103;
Best Local Similarity 43.3%; Pred. No. 1.1e-16;
Matches 45; Conservative 19; Mismatches 34; Indels 6; Gaps 3;
QY 5 APSVFIPPPDEQLKSGT-ASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63
DB 5 APTTLFPSPKEELNEATKATLVCLINDFVSPVVDWIDGTRSG---ETTPAQRSN 61
QY 64 STYLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 107
DB 62 SQYNASSYLSASDWSHETTCRVTHNGTS--ITKTKRSEC 103
RESULT 10
KAC_RANCA STANDARD; PRT; 108 AA.
AC P11272;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig light chain C region.
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RX MEDLINE=89039916; PubMed=3141797;
RA Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of the constant region of immunoglobulin light
chains from Rana catesbeiana."
RL Mol. Immunol. 25:695-703(1988).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93135; K3FG.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1
FT DISULFID 28 85
FT DISULFID 103 103
FT VARIANT 90
FT VARIAT 90
SQ SEQUENCE 103 AA; 11361 MW; 77BF341B511B91B2 CRC64;
Query Match 41.8%; Score 231; DB 1; Length 103;
Best Local Similarity 43.3%; Pred. No. 1.1e-16;
Matches 45; Conservative 19; Mismatches 34; Indels 6; Gaps 3;
QY 5 APSVFIPPPDEQLKSGT-ASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKD 63
DB 5 APTTLFPSPKEELNEATKATLVCLINDFVSPVVDWIDGTRSG---ETTPAQRSN 61
QY 64 STYLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 107
DB 62 SQYNASSYLSASDWSHETTCRVTHNGTS--ITKTKRSEC 103

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FT DISULFID 13 106
FT DISULFID 28 86
FT VARIANT 47 47
SQ SEQUENCE 108 AA; 11808 MW; 60B18F7AF1411F6C CRC64;
Query Match 40.7%; Score 225; DB 1; Length 108;
Best Local Similarity 48.0%; Pred. No. 8.1e-16;
Matches 49; Conservative 16; Mismatches 33; Indels 2; Gaps 2;
QY 6 PSVFIPPPDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDST 65
DB 7 PTVSYCPSPLEQNSGSASTVCLVDVKFYFGGAQVTKGDKNVISGVTSDKIKD-KDNT 65
QY 66 YLSLSLTLSKADYKHKYACEVTHQGLSPVTKSFNRGEC 107
DB 66 YSMSSTLTMSGEEF-KYSTMTCEVHTPTLTALAKSFQTSSEC 106
RESULT 11
KACS_RABIT STANDARD; PRT; 103 AA.
AC P01841;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa-95 chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=83178897; PubMed=6404296;
RA Ayadi H., Dutka S., Paroutaud P., Strosberg A.D.;
RT "Partial amino acid sequence of a rabbit immunoglobulin light chain
of allotype B5."
RL Biochemistry 22:993-998(1983).
RN [2]
RP SEQUENCE OF 4-103.
RX MEDLINE=82057807; PubMed=6795448;
RA Chersi A., Alexander C.B., Mage R.G.;
RT "Partial primary structure of the immunoglobulin light chain constant
region of a single rabbit of B5 allotype."
RL Mol. Immunol. 17:1515-1523(1980).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A30480; K5RB.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0407; IGC1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1
FT DISULFID 26 85
FT DISULFID 103 103
FT CONFLICT 5 5
FT CONFLICT 14 14
FT CONFLICT 21 21
FT CONFLICT 82 82
FT CONFLICT 87 88
SQ SEQUENCE 103 AA; 10945 MW; F33800791B031DD3 CRC64;
Query Match 40.4%; Score 223.5; DB 1; Length 103;
Best Local Similarity 44.7%; Pred. No. 1.1e-15;
Matches 46; Conservative 19; Mismatches 35; Indels 3; Gaps 3;
QY 5 APSVFIPPPDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDS 64
DB 4 APTVLIFPPAQLATGAVTIVCVANKYFP-DGTVTWEVDGKPLTTGTGTSKTPQNSDDC 62

```


RT immunoglobulin lambda-chains.";
 RL Biochem. J. 197;177-183(1981)
 CC -!- MISCELLANEOUS: THIS LAMEDA CHAIN EXPRESSES THE C7 ALLOTYPIC
 CC -!- SPECIFICITY.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; Igcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 6 100 IG-LIKE.
 FT DISULFID 27 86
 FT DISULFID 104 104 INTERCHAIN (WITH HEAVY CHAIN).
 SQ SEQUENCE 105 AA; 11484 MW; B427513272E8663D CRC64;

Query Match 36.8%; Score 203.5; DB 1; Length 105;
 Best Local Similarity 44.3%; Pred. No. 1.1e-13;
 Matches 47; Conservative 15; Mismatches 33; Indels 11; Gaps 4;
 QY 6 PSVIFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS--QESVTEQDSKD 63
 DB 6 PSVILFPSPSELKDKATLVCLISDFYPRTVKYNKAD-----GNSVTQGVDTTPSKQ 60
 QY 64 ST--YSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SNKYAASSFLHLTANQKWSQSVTCQVTHEG--HTVEKSLAPAE 104

RESULT 15
 LAC1 RAT STANDARD; PRT; 104 AA.
 AC P20766;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig lambda-1 chain C region.
 OS Rattus norvegicus [Rat].
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 FN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87305594; PubMed=3114047;
 RA Steen M.L., Hellman L., Pettersson U.;
 RT "The immunoglobulin lambda locus in rat consists of two C lambda
 RL genes and a single v lambda gene.";
 RL Gene 55:75-84(1987).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
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 CC -----
 CC EMBL; M22520; AAA41419.1; ALT_INIT.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; Igcl; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1

FT DOMAIN 6 99 IG-LIKE.
 FT DISULFID 27 85
 FT DISULFID 103 103 INTERCHAIN (WITH HEAVY CHAIN).
 SQ SEQUENCE 104 AA; 11565 MW; CB71811F4BC878A CRC64;
 Query Match 34.4%; Score 190; DB 1; Length 104;
 Best Local Similarity 39.0%; Pred. No. 2.4e-12;
 Matches 41; Conservative 20; Mismatches 38; Indels 6; Gaps 3;
 QY 4 AAPSVPFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGNSQESVTEQDSK 62
 DB 4 ATPSVTLFPSPSELKDKATLVCMVDFYPGVMTVVMKADGTPITQGVETTPQPKQNK 63
 QY 63 DSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
 DB 64 ---YMAISYLLLTAKAWETHSNYSQVTHE--ENTVEKSLAPAE 103

Search completed: January 13, 2004, 12:39:29
 Job time : 5.67249 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 19.1572 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFIPPPSDEQLKS.....EVTHQGLSSPVTKSFNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	234	4	Q8NEK1
2	553	100.0	239	4	Q8TCD0
3	549	99.3	239	4	Q8NEK0
4	352	63.7	233	11	Q91WS9
5	352	63.7	234	11	Q8R028
6	352	63.7	234	11	Q91WF8
7	352	63.7	234	11	Q8R062
8	352	63.7	234	11	Q8VCP0
9	352	63.7	235	11	Q91W12
10	352	63.7	238	11	Q8VCI6
11	352	63.7	238	11	Q99M37
12	352	63.7	239	11	Q8VC55
13	352	63.7	239	11	Q8K0F8
14	347	62.7	214	11	Q91IA5
15	211.5	38.2	105	4	Q8TJ35
16	211.5	38.2	233	4	Q8TBC9
					Q8TBC9 homo sapien

17	211.5	38.2	236	4	Q8NEJ1
18	210.5	38.1	130	11	Q9D8W4
19	208.5	37.7	233	4	Q8N5F4
20	208.5	37.7	234	4	Q8N355
21	208.5	37.7	237	4	Q8WUK4
22	208.5	37.7	237	4	Q8WTU6
23	208.5	37.7	240	4	Q8WUK3
24	199.5	36.1	235	11	Q99M11
25	192.5	34.8	233	4	Q96169
26	192.5	34.8	236	4	Q96E61
27	174	31.5	105	11	Q99JCL
28	159.5	28.8	473	11	Q9D8L4
29	153.5	27.8	468	11	Q99L31
30	153.5	27.8	473	11	Q99L25
31	151	27.3	473	4	Q8TC63
32	149	26.9	509	4	Q8NF17
33	149	26.9	521	4	Q8N4Y9
34	148	26.8	471	4	Q8TC77
35	148	26.8	701	4	Q96PQ8
36	144	26.0	473	11	Q91Z05
37	144	26.0	474	11	Q8R3H6
38	143	25.9	463	11	Q99LC4
39	142	25.7	437	11	Q91IA4
40	142	25.7	469	11	Q8R3V9
41	139.5	25.2	337	6	Q95M34
42	136	24.6	613	11	Q8VCX7
43	134	24.2	584	13	Q90544
44	127.5	23.1	267	13	Q90529
45	127.5	23.1	268	13	Q90524

ALIGNMENTS

RESULT 1
Q8NEK1 PRELIMINARY; PRT; 234 AA.

ID Q8NEK1; AC Q8NEK1; DT 01-OCT-2002 (TREMRELrel. 22, Created)
DT 01-OCT-2002 (TREMRELrel. 22, Last sequence update)
DT 01-VAR-2003 (TREMRELrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC030813; AAH30813.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25530 MW; 63168DEFD132F8 CRC64;
Query Match 100.0%; Score 553; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPPSDEQLKSCTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQ 60
Db 128 RTVAAPSVFIPPPSDEQLKSCTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQ 187
QY 61 SKDSTYLSLTLSKADYKHKYACEVTHQGSSPVTXSFNRGEC 107

SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
 Query Match 99.3%; Score 549; DB 4; Length 239;
 Best Local Similarity 99.1%; Pred. No. 4.7e-49;
 Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1 RTVAAPSVFIPTPPSDQLKSGTASVWCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQD 60
 DB 133 RTVAAPSVFIPTPPSDQLKSGTASVWCLLNFFYPREAKVQMKVDNTLQSGNSQESVTEQD 192
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 193 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
 Q91WS9 PRELIMINARY; PRT; 233 AA.
 AC Q91WS9
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 25.8 kDa protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013496; AAH13496.1; .
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA19A16EB CRC64;
 Query Match 63.7%; Score 352; DB 11; Length 233;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 85; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPTPPSDQLKSGTASVWCLLNFFYPREAKVQMKVDNALQSGNSQESVTEQD 60
 DB 127 RADAAPTSVFIPTPPSQLTSGGASVVCFLNFFPKDINVKWKIDGSRQGVLSNWTQD 186
 QY 61 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 DB 187 SKDSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRNEC 233

RESULT 5
 Q8R028 PRELIMINARY; PRT; 234 AA.
 AC Q8R028
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 25.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Strausberg R.;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027418; AAH27418.1; -
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_
 KW Hypothetical protein_
 KW Hypothetical protein_
 SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 128 RADAAPTWSIFPPSDEQLKSGTASVVCFLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187
 QY 61 SKDSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 107
 DB 188 SKDSTYSMSSTLTLTQDEYERHNSYTCEATHKSTSPIVKSFNRNEC 234

RESULT 8
 Q8VCF0 Q8VCF0 PRELIMINARY; PRT; 234 AA.
 ID Q8VCF0
 AC Q8VCF0;
 DT 01-11-2002 (TREMELrel. 20, Created)
 DT 01-11-2002 (TREMELrel. 20, Last sequence update)
 DE 01-11-2002 (TREMELrel. 23, Last annotation update)
 DE Hypothetical 25.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019474; AAH19474.1; -
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 63.7%; Score 352; DB 11; Length 234;
 Best Local Similarity 60.7%; Pred. No. 1.3e-28;
 Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 DB 128 RADAAPTWSIFPPSDEQLKSGTASVVCFLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 187
 QY 61 SKDSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 107
 DB 188 SKDSTYSMSSTLTLTQDEYERHNSYTCEATHKSTSPIVKSFNRNEC 234

RESULT 9
 Q91W12

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ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Unknown (Protein for MGC:16582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP NCBI_TaxID=10090;
RQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 63.7%; Score 352; DB 11; Length 235;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 129 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKIDINVKWIDGSEKQNGVLSWTDQD 186

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 189 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNREC 235

RESULT 10
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16;
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP NCBI_TaxID=10090;
RQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 358C08E3DE5414AD CRC64;

Query Match 63.7%; Score 352; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKIDINVKWIDGSEKQNGVLSWTDQD 191

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 189 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNREC 235

RESULT 11
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37;
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP NCBI_TaxID=10090;
RQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 63.7%; Score 352; DB 11; Length 238;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKIDINVKWIDGSEKQNGVLSWTDQD 191

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 192 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNREC 238

RESULT 12
Q8VC55 PRELIMINARY; PRT; 239 AA.
ID Q8VC55;
AC Q8VC55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP NCBI_TaxID=10090;
RQ SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 132 RADAAPTQSVIFPPSSQSLTSGGASVVCFLNNFYPKIDINVKWIDGSEKQNGVLSWTDQD 191

QY 61 SKDSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
DB 192 SKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPIVKSFNREC 238
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Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTQSVIPPPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTQDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 239

RESULT 13
Q8KOF8 PRELIMINARY; PRT; 239 AA.
AC Q8KOF8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Breast tumor;
RC Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC031498; AA31498.1; -.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SMC0409; IG; 2.
DR SMART; SMC0407; IG_C1; 1.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26366 MW; D7B884398AA341F0 CRC64;

Query Match 63.7%; Score 352; DB 11; Length 239;
Best Local Similarity 60.7%; Pred. No. 1.4e-28;
Matches 65; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 133 RADAAPTQSVIPPPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 192
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 193 SKDSTYMSSTLTLTQDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 239

RESULT 14
Q9RIAS PRELIMINARY; PRT; 214 AA.
AC Q9RIAS;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RA "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
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RT single chain antibody (scFV).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF152371; AAD40242.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SMC0406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 214 214
FT NON_TER 1
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 62.7%; Score 347; DB 11; Length 214;
Best Local Similarity 59.8%; Pred. No. 3.9e-28;
Matches 64; Conservative 15; Mismatches 28; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RADAAPTQSVIPPPSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQD 167
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYMSSTLTLTQDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214

RESULT 15
Q8TCJ5 PRELIMINARY; PRT; 106 AA.
AC Q8TCJ5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP667J0810.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Lymph node;
RC Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL713800; CAD28551.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SMC0407; IG_C1; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11265 MW; 145272BBE65F4565 CRC64;

Query Match 38.2%; Score 211.5; DB 4; Length 106;
Best Local Similarity 41.0%; Pred. No. 2e-14;
Matches 43; Conservative 26; Mismatches 31; Indels 5; Gaps 3;
QY 4 AAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNA-LOGNSQESVTEQDSK 62
DB 5 AAPSVFIPPPSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAG--VETTTFSKOS 62
QY 63 DSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 63 NKRYAASSYLSTLTPBQWKSHKSYSCQVTHEG--STVEKTVAPTEC 105

Search completed: January 13, 2004, 12:43:10
Job time : 20.1572 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 24.9511 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFPPSPDEQLKS.....EVTHQGLSSPVTKSPNRGEC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553	100.0	107	AAW40578	Human kappa CL dom
2	553	100.0	107	AAW50152	Human kappa light
3	553	100.0	107	AAW08745	Human kappa-CL dom
4	553	100.0	107	AAW92425	Human kappa protei
5	553	100.0	107	AAW827000	Human kappa CL dom
6	553	100.0	107	ABG311883	Human kappa CL dom
7	553	100.0	107	ABP98755	Human kappa light
8	553	100.0	143	ABP93559	Sequence of human
9	553	100.0	193	AAW52145	Humanised HMPGL I

10	553	100.0	201	20	AAW29770	p-selectin ligand
11	553	100.0	212	23	ABP51955	Humanised anti-CD1
12	553	100.0	213	17	AAW04301	Antibody fusion pr
13	553	100.0	213	22	AAE10510	Humanised high pot
14	553	100.0	213	22	AAE10512	Humanised high pot
15	553	100.0	213	22	AAE10514	Humanised high pot
16	553	100.0	213	22	AAE10516	Humanised high pot
17	553	100.0	213	22	AAE10518	Humanised high pot
18	553	100.0	213	22	AAE10520	Humanised high pot
19	553	100.0	213	22	AAE10522	Humanised high pot
20	553	100.0	213	22	AAE10524	Humanised high pot
21	553	100.0	213	22	AAE10526	Humanised high pot
22	553	100.0	213	22	AAE10528	Humanised high pot
23	553	100.0	213	23	ABP66563	Ganglioside GM2 an
24	553	100.0	213	23	ABP66565	Human RSV antibody
25	553	100.0	213	23	ABP66567	Human RSV antibody
26	553	100.0	213	23	ABP66569	Human RSV antibody
27	553	100.0	213	23	ABP66571	Human RSV antibody
28	553	100.0	213	23	ABP66573	Human RSV antibody
29	553	100.0	213	23	ABP66575	Human RSV antibody
30	553	100.0	213	23	ABP66577	Human RSV antibody
31	553	100.0	213	23	ABP66579	Human RSV antibody
32	553	100.0	213	23	ABP66581	Human RSV antibody
33	553	100.0	213	23	ABP66583	Human RSV antibody
34	553	100.0	213	23	ABP66585	Human RSV antibody
35	553	100.0	213	23	ABP66587	Human RSV antibody
36	553	100.0	213	23	ABP66589	Human RSV antibody
37	553	100.0	213	23	ABP66591	Human RSV antibody
38	553	100.0	213	23	ABP66593	Human RSV antibody
39	553	100.0	213	23	ABP66595	Human RSV antibody
40	553	100.0	213	23	ABP66597	Human RSV antibody
41	553	100.0	213	23	ABP66599	Human RSV antibody
42	553	100.0	213	23	ABP66601	Human RSV antibody
43	553	100.0	213	23	ABP66603	Human RSV antibody
44	553	100.0	213	23	ABP66605	Human RSV antibody
45	553	100.0	213	23	ABP66607	Human RSV antibody

ALIGNMENTS

RESULT 1

AAW40578
ID AAW40578 standard; protein; 107 AA.

XX AC AAW40578;

XX DT 21-JUL-1998 (first entry)

XX DE Human kappa CL domain protein fragment.

XX KW Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;

XX KW disorder; salvage receptor binding epitope; cell adherence interaction;

XX KW lymphocyte; T cell inflammatory response.

XX OS Homo sapiens.

XX PN US5739277-A.

XX PD 14-APR-1998.

XX PF 14-APR-1995; 95US-0422101.

XX PR 14-APR-1995; 95US-0422101.

XX PA (GETH) GENENTECH INC.

XX PI Presta LG, Snedecor BR;

XX DR WPI, 1998-250490/22.

XX PT Polypeptide(s) that are not Fc fragments and have an increased

PT half-life - are useful for the treatment of LFA-1 mediated disorders

XX Disclosure; Fig 2; 38pp; English.

XX This protein fragment is derived from a human immunoglobulin kappa CL

CC domain and is used to describe a novel method to produce polypeptides

CC which contain an epitope from the Fc region of an IgG molecule and a

CC mutated salvage receptor binding epitope. They are useful for the

CC treatment of LFA-1 mediated disorders. These are conditions caused by

CC cell adherence interactions involving the LFA-1 receptor on lymphocytes,

CC e.g. T cell inflammatory responses. The mutated salvage receptor sequence

CC in the polypeptides means that they have increased in vivo circulatory

CC half-lives when compared to normal Fc regions of IgG molecules.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 19; Length 107;

Best Local Similarity 100.0%; Pred. No. 6.4e-49;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTVLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTVLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 2

AAV50152

ID AAY50152 standard; Protein; 107 AA.

XX AAY50152;

DT 31-JAN-2000 (first entry)

XX Human kappa light chain constant region.

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;

KW humanisation; complementarity determining region; CDR; CDR grafting;

KW reshaped; reactive stroma; fibroblast; epithelial cancer;

KW diagnosis; immune response; framework sequence; constant region;

KW variable region; producibility; treatment; cancer; colorectal; lung;

KW breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;

KW detection; wound healing; skin inflammation; tumour; immunogenicity;

KW light chain.

XX Homo sapiens.

XX EP953639-A1.

XX 03-NOV-1999.

XX 30-APR-1998; 98EP-0107925.

XX 30-APR-1998; 98EP-0107925.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;

PI Rettig WJ;

XX WPI; 1999-621833/54.

DR N-PSDB; AA232777.

XX New antibody protein, useful for treating cancer and for imaging

PT presence of activated stromal fibroblasts in healing wound or inflamed

PT skin -

XX Disclosure; Fig 20; 143pp; English.

XX This sequence represents a human kappa light chain, the cDNA of which

CC was used in the construction of a nucleotide encoding the light chain

CC of a human reshaped monoclonal antibody F19. F19 (ATCC Accession number

CC HB 8269) is a murine monoclonal antibody against fibroblast

CC activation protein alpha (FAP). FAP is a cell surface molecule

CC of reactive stromal fibroblasts, and its induction is a highly

CC consistent molecular trait of the reactive stroma of many types of

CC epithelial cancer. Although F19 may be useful in vitro, e.g., for

CC diagnosis, its applications for in vivo use in humans are problematic

CC as it elicits a human anti-mouse response which reduces the efficacy of

CC the antibody in patients and impairs continued administration. The novel

CC human reshaped F19 was humanised by grafting the murine complementarity

CC determining regions (CDRs) of F19 onto human variable region framework

CC sequences, and then joining these "reshaped human" variable regions to

CC human constant regions. These modifications also result in the improved

CC producibility in eukaryotic cell culture systems as compared to a

CC chimeric antibody having the entire variable regions of F19 joined to

CC human constant regions. The human reshaped F19 antibody has low

CC immunogenicity for humans and is useful for treating cancers e.g.,

CC colorectal cancers, non-small cell lung cancers, breast cancers, head

CC and neck cancers, ovarian cancers, lung cancers, bladder cancers,

CC pancreatic cancers and metastatic cancers. It is also useful for the

CC detection of activated stromal fibroblasts in a healing wound, inflamed

CC skin or a tumour in a human patient.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 20; Length 107;

Best Local Similarity 100.0%; Pred. No. 6.4e-49;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

DB 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTVLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

DB 61 SKDSTVLSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 107

RESULT 3

AAV08745

ID AAY08745 standard; Protein; 107 AA.

XX AAY08745;

XX 10-AUG-1999 (first entry)

XX Human Kappa-CL domain.

XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;

KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;

KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;

KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;

KW antibody.

XX Homo sapiens.

XX US5914112-A.

XX 22-JUN-1999.

XX 22-JAN-1997; 97US-0788800.

XX 23-JAN-1996; 96US-0093038.

XX 22-JAN-1997; 97US-0788800.

XX (GETH) GENENTECH INC.

XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.

XX Bednar WM, Gross CE, Thomas GR;

XX WPI; 1999-370483/31.

XX Anti-CD18 antibodies in stroke

XX Disclosure, Fig 4A-B; 25pp; English.

XX This invention describes a method for improving the clinical outcome in focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 to bind to endothelium, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD18/CD18 complex. This sequence represents the human kappa-CL domain which is used to illustrate the method of the invention.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 20; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
AAW92425
ID AAW92425 standard; peptide; 107 AA.

AC AAW92425;

DT 23-APR-1999 (first entry)

DE Human Kappa protein CL domain.

XX Antibody; salvage receptor binding epitope; Fab; F(ab')₂; immunoglobulin; CH region; CL region; kidney; FC region; CH1 domain; CH2 domain; Igg; kappa protein; renal clearance rate; circulatory half-life.

OS Homo sapiens.

XX US5869046-A.

PN 09-FEB-1999.

PD 14-APR-1995; 95US-0422092.

PF 14-APR-1995; 95US-0422092.

PR 14-APR-1995; 95US-0422092.

XX (GETH) GENENTECH INC.

PA Presta LG, Snedecor BR;

PI WPI; 1999-152694/13.

DR Production of antibody fragments with reduced renal clearance - by introducing salvage receptor binding epitope into CH1 or CL region

PT Disclosure; Column 55-58; 38pp; English.

XX This invention describes a method for preparing a variant Fab or F(ab')₂ polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleared from the kidneys and does not contain an Igg FC region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an Igg FC region. The polypeptides have a reduced renal

CC clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the invention.

XX Sequence 107 AA;

QY Query Match 100.0%; Score 553; DB 20; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYKVVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
AAB27000
ID AAB27000 standard; Protein; 107 AA.

AC AAB27000;

DT 25-JAN-2001 (first entry)

XX Human kappa CL domain.

XX Salvage receptor binding epitope; immunomodulator; LFA-1 agonist; mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease; psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair; inflammation; vaccine.

OS Homo sapiens.

XX US6121022-A.

PN 19-SEP-2000.

PD 14-APR-1995; 95US-0422112.

PF 14-APR-1995; 95US-0422112.

PR (GETH) GENENTECH INC.

PA Presta LG, Snedecor BR;

PI WPI; 2000-610925/58.

DR New nucleic acid encoding new modified polypeptides with increased circulatory half-life useful for preventing/treating LFA-1-mediated disorders, e.g. reducing inflammatory responses or inducing tolerance to immunostimulants

XX Disclosure; Fig 2; 38pp; English.

XX The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain or an Ig-like constant domain, and a salvage receptor binding epitope within the Ig or Ig-like domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an FC region of an Ig molecule. The modified polypeptides are useful for preventing or treating LFA-1-mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated diseases, B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources.

XX Sequence 107 AA;

Query Match 100.0%; Score 553; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||
 Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||

Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||
 Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||

RESULT 6
 ID ABG31883 standard; protein; 107 AA.
 XX AC ABG31883;
 XX DT 05-NOV-2002 (first entry)
 XX DE Human kappa CL domain.
 XX KW Human; kappa CL domain; cerebral blood flow; infarct size;
 KW focal ischaemic stroke; main cerebral artery;
 KW tissue plasminogen activator; anti-CD18 antibody; stroke;
 KW acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.
 XX OS Homo sapiens.
 XX US2002081294-A1.
 XX PD 27-JUN-2002.
 XX PF 20-DEC-2000; 2000US-0811384.
 XX PR 23-JAN-1996; 96US-093038P.
 PR 17-FEB-1999; 99US-0251652.
 PR 22-JAN-1997; 97US-0788800.
 XX PA (GETH) GENENTECH INC.

XX PI Bednar MM, Gross CE, Thomas GR, Gross LJ;
 XX WPI; 2002-626528/67.
 XX PT Increasing cerebral blood flow and/or reducing infarct size in focal
 PT ischaemic stroke using anti-CD18 antibody and tissue plasminogen
 PT activator is useful to improve clinical outcome in acute ischaemic
 PT stroke -
 XX PS Disclosure; Fig 4; 27pp; English.
 XX CC The invention relates to a method of increasing cerebral blood flow and/
 CC or reducing infarct size in focal ischaemic stroke caused by obstruction
 CC of a main cerebral artery in a human, comprising co-administering tissue
 CC plasminogen activator and anti-CD18 antibody about 3-5 hours after the
 CC stroke. The method is used to improve the clinical outcome in acute
 CC ischaemic stroke and to provide an alternative to thrombolytic therapy
 CC for treating thromboembolic stroke, particularly where thrombolytic
 CC therapy has been unsuccessful or is contra-indicated. The present
 CC sequence represents the human kappa CL domain used in the method of the
 CC invention.

XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 23; Length 107;
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||

Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||
 Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||
 Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 |||||

RESULT 7
 ID ABB98755 standard; Protein; 107 AA.
 XX AC ABB98755;
 XX DT 23-JAN-2003 (first entry)
 XX DE Human kappa light constant chain.
 XX KW Human; cytostatic; antitumour; immunosuppressive; antiallergic;
 KW humanised; antibody; fibroblast activation protein alpha; FAPalpha;
 KW cancer; monoclonal antibody F19; colorectal cancer;
 KW non-small cell lung carcinoma; breast cancer; pancreatic cancer;
 KW tumour; systemic autoimmune disease; allergy; light chain;
 XX constant region.
 XX OS Homo sapiens.
 XX WO200283171-A2.
 XX PD 24-OCT-2002.
 XX PF 11-APR-2002; 2002WO-EP04041.
 XX PR 12-APR-2001; 2001US-283868P.
 XX PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX PI (BOEH) BOEHRINGER INGELHEIM PHARM INC.
 XX Amelsberg A, Scott A, Tanswell P;
 XX WPI; 2003-058609/05.
 XX DR N-PSDB; ABV74601.

XX PT Use of a humanized antibody which specifically binds to fibroblast
 PT activation protein alpha for manufacturing a medicament for treating
 PT cancer -
 XX Claim 7; Page 55; 57pp; English.

XX CC The present invention relates to the use of a humanised antibody (I),
 CC which specifically binds to fibroblast activation protein alpha
 CC (FAPalpha), for manufacturing a medicament for treating cancer. (I) has
 CC the complementary determining region (CDR) of the monoclonal antibody
 CC F19, but has framework modifications resulting in improved producibility
 CC in host cells as compared to a chimeric antibody having the variable
 CC regions of F19 and foreign constant regions. To generate (I), a chimeric
 CC antibody was constructed having variable regions of the light and heavy
 CC chains of F19 and human light and heavy constant regions. (I) is useful
 CC for treating a patient suffering from a pathological condition
 CC characterised by expression of FAPalpha, such as colorectal cancer,
 CC non-small cell lung carcinoma, breast cancer, pancreatic cancer, tumours,
 CC systemic autoimmune diseases and allergies. The present sequence is
 CC human kappa light constant chain which was used to produce (I).

XX SQ Sequence 107 AA;
 Query Match 100.0%; Score 553; DB 24; Length 107;
 Best Local Similarity 100.0%; Pred. No. 6.4e-49;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||
 Db 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 |||||

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
 AAP93559
 ID AAP93559 standard; protein; 143 AA.

XX AC AAP93559;
 XX DT 25-MAR-2003 (updated)
 XX DT 28-JAN-1991 (first entry)
 XX DE Sequence of human kappa light chain fragment.

XX KW HIV; antiviral; therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Region 1..37
 XX FT /label=
 XX FT /note="light variable and joining"
 XX FT 38..38
 XX FT /note="light constant"
 XX FT 37..38
 XX FT /note="insert site"

XX PN WO902922-A.

XX XX 06-APR-1989.

XX XX 03-OCT-1988; 88WO-US03414.

XX XX 02-OCT-1987; 87US-0104329.

XX XX 28-SEP-1988; 88US-0250785.

XX PA (GETH) GENENTECH INC.

XX PI Capon DJ, Gregory TJ;

XX XX WPI; 1989-1114397/15.

XX DR P-PSDB; AAP93559.

XX XX New nucleic acid sequences encoding adhesion, esp. CD4, variants -
 PT partic. with trans-membrane domain inactivated or fused to other
 PT peptide, useful esp. for treating HIV infections

XX PS Example; Figure Fig 5; 78pp; English.

XX CC It is employed in the prepn. of CD4 fusions. The insert site is
 CC given in the Features Table. CD4 fusion proteins can have antiviral and
 CC immunomodulatory activity are esp. useful for treating HIV infections,
 CC regardless of genetic variation within the virus. They and antibodies
 CC raised against them can also be used diagnostically for assaying adhesions
 CC and their ligands.

XX CC (Updated on 25-MAR-2003 to correct PR field.)

XX CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 143 AA;

Query Match 100.0%; Score 553; DB 10; Length 143;
 Best Local Similarity 100.0%; Pred. No. 9.2e-49;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 60
 DB 37 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 96

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 DB 97 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 143

RESULT 9
 AAM52145
 ID AAM52145 standard; Protein; 193 AA.

XX AC AAM52145;

XX DT 05-FEB-2002 (first entry)

XX DE Humanised HMFG1 light chain.

XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 XX cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX OS Synthetic.

XX PN WO200174905-A1.

XX PD 11-OCT-2001.

XX PF 26-MAR-2001; 2001WO-GB01324.

XX PR 03-APR-2000; 2000GB-0008049.

XX PR 02-OCT-2000; 2000US-237159P.

XX PA (ANTI-) ANTISOMA RES LTD.

XX PI Young RJ;

XX DR WPI; 2001-662969/76.

XX PT Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity

XX PS Claim 20; Figure 3; 176pp; English.

XX CC The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 553; DB 22; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.3e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 60
 DB 87 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNFPYPRKQVQKVDNALQSGNSQESVTEQD 146

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 DB 147 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 193

RESULT 10
 AAY29770
 ID AAY29770 standard; Protein; 201 AA.

XX AC AAY29770;

XX DT 04-NOV-1999 (first entry)

XX DE P-selectin ligand and kappa chain constant region fusion protein.
 XX Human; P-selectin ligand; glycoprotein; fusion protein; infection;


```
Db 106 RTVAAPSVFIIPPDEQLKSGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQD 165
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 166 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 12
AAW04301
ID AAW04301 standard; Protein; 213 AA.
XX
AC AAW04301;
XX
DT 25-MAR-2003 (updated)
DT 14-FEB-1997 (first entry)
XX
DE Antibody fusion protein.
XX
KW Antibody; fusion protein; recombinant antibody; tumour therapy;
KW prodrug.
XX
OS Synthetic.
XX
PN EP737747-A2.
XX
PD 16-OCT-1996.
XX
PF 13-MAR-1996; 96EP-0103913.
XX
PR 11-APR-1995; 95DE-1013676.
XX
PA (BEHW ) BEHRINGWERKE AG.
XX
FI Boeslet K, Czech J, Oppen M;
XX
DR WPI; 1996-457328/46.
XX
N-PSDB; AAT38397.
XX
Prod. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion
PT protein - by cytoplasmic expression in thio:redoxin:reductase
PT deficient E. coli
XX
Example 1; Figure 5a; 12pp; German.
XX
Production of recombinant antibodies (Ab), Ab fragments or Ab
CC fragment/enzyme fusion proteins can be used for tumour therapy,
CC especially when the fusion protein comprises a tumour-specific
CC Ab fragment and an enzyme capable of converting a non-toxic prodrug
CC to a toxic drug. The fusion proteins are constructed in expression
CC vectors and expressed in thiorodoxinreductase deficient E.coli,
CC allowing expression products to be isolated in soluble functional
CC form without renaturation. The Ab fragment is an FAb fragment or an
CC antigen binding region. In the fusion protein, the Ab component is
CC humanised and the enzyme component is a human cytoplasmic enzyme.
CC This fusion protein comprises the antibody constant and variable
CC light chain regions.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 17; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPDEQLKSGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIIPPDEQLKSGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQD 166
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
AAE10512
ID AAE10512 standard; Protein; 213 AA.
XX
AC AAE10512;
XX
```

```
RESULT 13
AAE10510
ID AAE10510 standard; Protein; 213 AA.
XX
AC AAE10510;
XX
DT 10-DEC-2001 (first entry)
XX
DE Humanised high potency antibody clone 25 full length light chain.
XX
KW Human; light chain; respiratory syncytial virus infection; virucide;
KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
KW cancer cell; toxic substance.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200164751-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US06815.
XX
PR 01-MAR-2000; 2000US-0186252.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
XX
WPI; 2001-582150/65.
XX
High potency recombinant antibody, useful for preventing and treating
PT diseases induced or caused by viruses, especially respiratory syncytial
PT virus and parainfluenza virus, has high kinetic association rate
PT constant
XX
Claim 23; Page 75-76; 98pp; English.
XX
The invention relates to a high potency antibody including its
CC immunologically active portions, fragments and segments other than
CC vitaxin. The antibody has increased potency, high rate constant for
CC antibody-antigen complex formation and high affinity for any desired
CC antigen. The high potency antibody is also useful for nullifying or
CC ameliorating the effects of addictive drugs, such as cocaine. The high
CC potency has specificity for antigenic determinants found on microbes
CC such as viruses, bacteria or fungi, antigens found on cancer cells and
CC toxic substances or product of toxic substances. The high potency
CC antibody is useful for preventing or treating a disease caused by a
CC virus such as respiratory syncytial virus (RSV) and parainfluenza
CC virus (PIV). The present sequence is humanised high potency antibody
CC full length light chain variable region.
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 553; DB 22; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIIPPDEQLKSGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQD 60
DB 107 RTVAAPSVFIIPPDEQLKSGTASVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQD 166
QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 167 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 14
AAE10512
ID AAE10512 standard; Protein; 213 AA.
XX
AC AAE10512;
XX
```

DT 10-DEC-2001 (first entry)
 XX Humanised high potency antibody clone 26 full length light chain.
 DE
 DE
 KW Human; light chain; respiratory syncytial virus infection; virucide;
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;
 KW cancer cell; toxic substance.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164751-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 01-MAR-2001; 2001WO-US06815.
 XX
 XX 01-MAR-2000; 2000US-0186252.
 XX
 XX (MEDI-) MEDIMUNE INC.
 PA
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
 XX WPI; 2001-582150/65.
 XX
 XX High potency recombinant antibody, useful for preventing and treating
 PT diseases induced or caused by viruses, especially respiratory syncytial
 PT virus and parainfluenza virus, has high kinetic association rate
 PT constant -
 XX
 PS Claim 23; Page 78-79; 98pp; English.
 XX
 CC The invention relates to a high potency antibody including its
 CC immunologically active portions, fragments and segments other than
 CC vitaxin. The antibody has increased potency, high rate constant for
 CC antibody-antigen complex formation and high affinity for any desired
 CC antigen. The high potency antibody is also useful for nullifying or
 CC ameliorating the effects of addictive drugs, such as cocaine. The high
 CC potency has specificity for antigenic determinants found on microbes
 CC such as viruses, bacteria or fungi, antigens found on cancer cells and
 CC toxic substances or product of toxic substances. The high potency
 CC antibody is useful for preventing or treating a disease caused by a
 CC virus such as respiratory syncytial virus (RSV) and parainfluenza
 CC virus (PIV). The present sequence is humanised high potency antibody
 CC full length light chain variable region.
 XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 553; DB 22; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 107
 Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 213
 QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 107
 Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 213
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KW cancer cell; toxic substance.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200164751-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 01-MAR-2001; 2001WO-US06815.
 XX
 XX 01-MAR-2000; 2000US-0186252.
 XX
 XX (MEDI-) MEDIMUNE INC.
 PA
 PI Young JF, Koenig S, Johnson LS, Huse WD, Wu H, Watkins JD;
 XX WPI; 2001-582150/65.
 XX
 XX High potency recombinant antibody, useful for preventing and treating
 PT diseases induced or caused by viruses, especially respiratory syncytial
 PT virus and parainfluenza virus, has high kinetic association rate
 PT constant -
 XX
 PS Claim 23; Page 80-81; 98pp; English.
 XX
 CC The invention relates to a high potency antibody including its
 CC immunologically active portions, fragments and segments other than
 CC vitaxin. The antibody has increased potency, high rate constant for
 CC antibody-antigen complex formation and high affinity for any desired
 CC antigen. The high potency antibody is also useful for nullifying or
 CC ameliorating the effects of addictive drugs, such as cocaine. The high
 CC potency has specificity for antigenic determinants found on microbes
 CC such as viruses, bacteria or fungi, antigens found on cancer cells and
 CC toxic substances or product of toxic substances. The high potency
 CC antibody is useful for preventing or treating a disease caused by a
 CC virus such as respiratory syncytial virus (RSV) and parainfluenza
 CC virus (PIV). The present sequence is humanised high potency antibody
 CC full length light chain variable region.
 XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 553; DB 22; Length 213;
 Best Local Similarity 100.0%; Pred. No. 1.5e-48;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 QY 61 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 107
 Db 167 SKDSTYSLSTLTLSKADYERKHVKYACEVTHQGLSPVTKSFNRGEC 213
 Search completed: January 13, 2004, 12:38:27
 Job time : 24.9511 secs

RESULT 15
 AA010514
 ID AA010514 standard; Protein; 213 AA.
 XX
 AC AA010514;
 XX
 XX 10-DEC-2001 (first entry)
 XX
 XX Humanised high potency antibody clone 18 full length light chain.
 DE
 DE
 KW Human; light chain; respiratory syncytial virus infection; virucide;
 KW parainfluenza virus; therapy; high potency antibody; drug; cocaine;

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OM protein - protein search, using sw model

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(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-99

Perfect score: 553

Sequence: 1 RTVAAPSVFPPSDEQLKS.....EVTHQGLSSFTKSNRGC 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	553	100.0	107	9	US-09-811-384-5
2	553	100.0	107	11	US-09-990-586-99
3	553	100.0	107	11	US-09-990-586-99
4	553	100.0	107	12	US-10-159-006-20
5	553	100.0	107	12	US-10-310-113-166
6	553	100.0	107	12	US-10-310-113-168
7	553	100.0	107	12	US-10-230-880-97
8	553	100.0	107	12	US-10-230-880-99
9	553	100.0	107	12	US-10-366-709-54
10	553	100.0	107	15	US-10-121-454-18
11	553	100.0	107	15	US-10-269-805-67
12	553	100.0	212	12	US-10-320-231A-77
13	553	100.0	212	14	US-10-011-125-5
14	553	100.0	213	9	US-09-796-848A-38
15	553	100.0	213	9	US-09-796-848A-40

Sequence 42, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 50, Appl
Sequence 52, Appl
Sequence 54, Appl
Sequence 209, App
Sequence 211, App
Sequence 211, App
Sequence 215, App
Sequence 217, App
Sequence 219, App
Sequence 221, App
Sequence 223, App
Sequence 225, App
Sequence 227, App
Sequence 229, App
Sequence 231, App
Sequence 233, App
Sequence 235, App
Sequence 237, App
Sequence 239, App
Sequence 241, App
Sequence 243, App
Sequence 245, App
Sequence 247, App
Sequence 251, App
Sequence 253, App
Sequence 255, App

16 553 100.0 213 9 US-09-796-848A-42
17 553 100.0 213 9 US-09-796-848A-44
18 553 100.0 213 9 US-09-796-848A-46
19 553 100.0 213 9 US-09-796-848A-48
20 553 100.0 213 9 US-09-796-848A-50
21 553 100.0 213 9 US-09-796-848A-52
22 553 100.0 213 9 US-09-796-848A-54
23 553 100.0 213 10 US-09-996-288-209
24 553 100.0 213 10 US-09-996-288-211
25 553 100.0 213 10 US-09-996-288-213
26 553 100.0 213 10 US-09-996-288-215
27 553 100.0 213 10 US-09-996-288-217
28 553 100.0 213 10 US-09-996-288-219
29 553 100.0 213 10 US-09-996-288-221
30 553 100.0 213 10 US-09-996-288-223
31 553 100.0 213 10 US-09-996-288-225
32 553 100.0 213 10 US-09-996-288-227
33 553 100.0 213 10 US-09-996-288-229
34 553 100.0 213 10 US-09-996-288-231
35 553 100.0 213 10 US-09-996-288-233
36 553 100.0 213 10 US-09-996-288-235
37 553 100.0 213 10 US-09-996-288-237
38 553 100.0 213 10 US-09-996-288-239
39 553 100.0 213 10 US-09-996-288-241
40 553 100.0 213 10 US-09-996-288-243
41 553 100.0 213 10 US-09-996-288-245
42 553 100.0 213 10 US-09-996-288-247
43 553 100.0 213 10 US-09-996-288-251
44 553 100.0 213 10 US-09-996-288-253
45 553 100.0 213 10 US-09-996-288-255

ALIGNMENTS

RESULT 1

US-09-811-384-5
; Sequence 5, Application US/09811384
; Patent No. US20020081294A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; Thomas, G. Roger
; Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/811,384
; FILING DATE: 20-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/251652
; FILING DATE: 17-FEB-2000
; APPLICATION NUMBER: 08/788800
; FILING DATE: 22-JAN-1997
; APPLICATION NUMBER: 60/093038
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1729C1
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-811-384-5

Query Match          100.0%; Score 553; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-09-990-586-97
; Sequence 97, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-97

Query Match          100.0%; Score 553; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-09-990-586-99
; Sequence 99, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-99

Query Match          100.0%; Score 553; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-10-159-006-20
; Sequence 20, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-20

Query Match          100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFPPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

Qy 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-10-310-113-166
; Sequence 166, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
```

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; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-166

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-10-310-113-168
; Sequence 168, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 168
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-168

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107
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; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-97

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYKVIYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-10-230-880-99
; Sequence 99, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-99

Query Match      100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 9
US-10-366-709-54
; Sequence 54, Application US/10366709
; Publication No. US20030219433A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, HANS
; APPLICANT: QU, ZHENGXING
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: ANTI-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
; FILE REFERENCE: 18733/115
; CURRENT APPLICATION NUMBER: US/10/366,709
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/356,132
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/416,232
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-709-54

Query Match 100.0%; Score 553; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 10
US-10-121-464-18
; Sequence 18, Application US/10121464
; Publication No. US20030103968A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies
; FILE REFERENCE: 1-1203ff
; CURRENT APPLICATION NUMBER: US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/283,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Antibody
US-10-121-464-18

Query Match 100.0%; Score 553; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 11
US-10-269-805-67
; Sequence 67, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLLNER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-67

Query Match 100.0%; Score 553; DB 15; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60
Qy 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 107

RESULT 12
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-77

Query Match 100.0%; Score 553; DB 12; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFI PPSPDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQD 60

Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
Qy 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 13
US-10-011-125-5
; Sequence 5, Application US/10011125
; Publication No. US20020142389A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804K1
; CURRENT APPLICATION NUMBER: US/10/011,125
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-5

Query Match 100.0%; Score 553; DB 14; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 106 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

Qy 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 166 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 212

RESULT 14
US-09-796-848A-38
; Sequence 38, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-38

Query Match 100.0%; Score 553; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 15
US-09-796-848A-40
; Sequence 40, Application US/09796848A
; Patent No. US20020098189A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
; FILE REFERENCE: 469201-526
; CURRENT APPLICATION NUMBER: US/09/796,848A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: U.S. 60/186,252
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Light chain of
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-40

Query Match 100.0%; Score 553; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

Qy 61 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTLSKADYKHKYKHYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: January 13, 2004, 13:13:46
Job time : 18.1013 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 9.25153 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-99
Perfect score: 553
Sequence: 1 RTVAAPSVFIPPSPDEQLKS.....EVTHGGLSSPVTKSNRGEK 107

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pdp.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pdp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	553	100.0	107	1	US-08-422-101-8	Sequence 8, Appli
2	553	100.0	107	1	US-08-422-091-8	Sequence 8, Appli
3	553	100.0	107	2	US-08-422-092-8	Sequence 8, Appli
4	553	100.0	107	2	US-08-788-800-5	Sequence 5, Appli
5	553	100.0	107	3	US-08-422-093-8	Sequence 8, Appli
6	553	100.0	107	3	US-08-422-112-8	Sequence 8, Appli
7	553	100.0	107	4	US-09-301-593-20	Sequence 20, Appli
8	553	100.0	213	3	US-08-630-820-6	Sequence 6, Appli
9	553	100.0	213	3	US-08-397-411-12	Sequence 12, Appli
10	553	100.0	214	1	US-08-458-516-12	Sequence 12, Appli
11	553	100.0	214	2	US-07-934-373C-24	Sequence 24, Appli
12	553	100.0	214	2	US-07-934-373C-39	Sequence 39, Appli
13	553	100.0	214	2	US-07-934-373C-40	Sequence 40, Appli
14	553	100.0	214	2	US-08-480-753-6	Sequence 6, Appli
15	553	100.0	214	2	US-08-788-800-11	Sequence 11, Appli
16	553	100.0	214	3	US-09-041-889-11	Sequence 11, Appli
17	553	100.0	214	3	US-08-437-642B-24	Sequence 24, Appli
18	553	100.0	214	3	US-08-437-642B-39	Sequence 39, Appli
19	553	100.0	214	3	US-08-437-642B-40	Sequence 40, Appli
20	553	100.0	214	3	US-08-837-058B-11	Sequence 11, Appli
21	553	100.0	214	3	US-09-097-309-2	Sequence 2, Appli
22	553	100.0	214	3	US-08-397-411-5	Sequence 5, Appli
23	553	100.0	214	3	US-09-097-171A-2	Sequence 2, Appli
24	553	100.0	214	4	US-09-247-352-4	Sequence 4, Appli
25	553	100.0	214	4	US-09-460-587-2	Sequence 2, Appli
26	553	100.0	214	4	US-09-679-397-1	Sequence 1, Appli
27	553	100.0	214	4	US-08-146-206C-24	Sequence 24, Appli

28	553	100.0	214	4	US-09-466-635-4	Sequence 4, Appli
29	553	100.0	214	4	US-09-680-148-1	Sequence 1, Appli
30	553	100.0	214	4	US-09-289-942A-6	Sequence 6, Appli
31	553	100.0	214	4	US-09-304-465A-1	Sequence 1, Appli
32	553	100.0	214	4	US-09-417-264-11	Sequence 11, Appli
33	553	100.0	214	5	PCT-US93-07832-24	Sequence 24, Appli
34	553	100.0	214	5	PCT-US93-07832-39	Sequence 39, Appli
35	553	100.0	214	5	PCT-US93-07832-40	Sequence 40, Appli
36	553	100.0	215	2	US-08-480-753-8	Sequence 8, Appli
37	553	100.0	218	2	US-08-887-352B-13	Sequence 13, Appli
38	553	100.0	218	2	US-08-887-352B-15	Sequence 15, Appli
39	553	100.0	218	2	US-08-887-352B-17	Sequence 17, Appli
40	553	100.0	218	2	US-08-887-352B-19	Sequence 19, Appli
41	553	100.0	218	3	US-08-887-352B-24	Sequence 24, Appli
42	553	100.0	218	3	US-08-466-151-9	Sequence 9, Appli
43	553	100.0	218	3	US-09-109-207C-13	Sequence 13, Appli
44	553	100.0	218	3	US-09-109-207C-15	Sequence 15, Appli
45	553	100.0	218	3	US-09-109-207C-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-422-101-8
; Sequence 8, Application US/08422101
; Patent No. 5732277
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,101
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-101-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 RTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYREAKVQMKVONALQSGNSQSVTQD 60
QY |||||

Db 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 2
US-08-422-091-8
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,091
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-091-8

Query Match 100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
Db 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 3
US-08-422-092-8
; Sequence 8, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,092
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-422-092-8

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
Db 1 RTVAAPSVFIPPSPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQD 60
QY 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 107

RESULT 4
US-08-788-800-5
; Sequence 5, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987r1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-788-800-5

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 5
US-08-422-093-8
Sequence 8, Application US/08422093
Patent No. 6096871
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-093-8

Query Match 100.0%; Score 553; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 6
US-08-422-112-8
Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-112-8

Query Match 100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 1 RTVAAPSVFIIPPSPDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 61 SKDSTYLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 7
US-09-301-593-20
Sequence 20, Application US/09301593A

Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Legier, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.189001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-20

Query Match 100.0%; Score 553; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

QY 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 8
US-08-630-820-6
Sequence 6, Application US/08630820
Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: Oppfer, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18749/306
TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-820-6

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
Db 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166

QY 61 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
Db 167 SKDSTYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213

RESULT 9
US-08-397-411-12
Sequence 12, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingsrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,593
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-12

Query Match 100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
| | | | |
Db 107 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 166
| | | | |
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
| | | | |
Db 167 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 213
| | | | |

RESULT 10
US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: CO, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-458-516-12
Query Match 100.0%; Score 553; DB 1; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
| | | | |
Db 108 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 167
| | | | |
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
| | | | |
Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
| | | | |

RESULT 11
US-07-934-373C-24
; Sequence 24, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-24

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 60
| | | | |
Db 108 RTVAAPSVIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQD 167
| | | | |
QY 61 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107
| | | | |
Db 168 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
| | | | |

RESULT 12
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-39

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 167

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 14
US-08-480-753-6
Sequence 6, Application US/08480753
Patent No. 5830675
GENERAL INFORMATION:
APPLICANT: Targan M.D., Stephan R.
TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS, OR
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendy A. Whiteford, Esq.
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whiteford, Wendy A.
REGISTRATION NUMBER: 36,964
REFERENCE/DOCKET NUMBER: P07 33571
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-753-6

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 167

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-39

Query Match 100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 60
DB 108 RTVAAPSVFPPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQD 167

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
DB 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 13
US-07-934-373C-40
Sequence 40, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 Db 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 15

US-08-788-800-11
 ; Sequence 11, Application US/08788800
 ; Patent No. 5914112
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednar, Martin M.
 ; APPLICANT: Thomas, G. Roger
 ; APPLICANT: Gross, Cordell E.
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/788,800
 ; FILING DATE: 22-Jan-1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0987r1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 214 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 US-08-788-800-11

Query Match 100.0%; Score 553; DB 2; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 60
 Db 108 RTVAAPSVFIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQD 167

QY 61 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107
 Db 168 SKDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: January 13, 2004, 12:46:35
 Job time : 9.25153 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:22:35 / Search time 23.8489 Seconds
(without alignments)
1326.664 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFASSTKGPSVFPLAPCSRST.....MHEALNHYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1743	99.4	327	1	G4HU	Ig gamma-4 chain C
2	1605.5	91.5	326	1	G2HU	Ig gamma-2 chain C
3	1590.5	90.7	330	1	G5HU	Ig gamma-1 chain C
4	1585	90.4	377	2	A50764	Ig gamma-3 chain C
5	1575	89.8	377	2	A23511	Ig gamma-3 chain C
6	1289.5	73.5	328	2	I47159	Ig gamma 2a chain
7	1283.5	73.2	328	2	I47160	Ig gamma 2b chain
8	1264.5	72.1	328	2	I47161	Ig gamma 1 chain C
9	1240.5	70.7	328	2	I47158	Ig gamma 1 chain C
10	1199	68.4	323	1	GHRB	Ig gamma chain C r
11	1189	68.4	472	2	S31459	Ig gamma-1 chain -
12	1185	66.6	470	2	S22080	Ig heavy chain pre
13	1158	66.0	329	1	G2GP	Ig gamma-2 chain C
14	1147	65.4	308	2	C30554	Ig heavy chain C r
15	1143	65.2	374	2	S69339	Ig heavy chain V r
16	1139.5	65.0	255	4	S31866	Ig gamma-1 chain C r
17	1129.5	64.4	234	2	PT0207	Ig gamma chain C r
18	1124	64.1	333	2	P80018	Ig gamma-2b chain C
19	1118.5	63.8	326	2	P80017	Ig gamma-1 chain C
20	1118.5	63.8	444	2	P44336	monoclonal antibod
21	1108.5	63.2	289	1	G3HUW1	Ig gamma-3 heavy c
22	1108	63.2	329	2	S00847	Ig gamma-2c chain C
23	1106.5	63.1	324	1	G1MS	Ig gamma-1 chain C
24	1106.5	63.1	330	1	G2MSA	Ig gamma-2a chain
25	1106.5	63.1	469	2	S37483	Ig gamma-2a chain C
26	11103	62.9	327	2	S06611	Ig gamma-2 chain C
27	1101.5	62.8	393	1	G1MSM	Ig gamma-1 chain C
28	1101.5	62.8	399	1	G2MSAB	Ig gamma-2a chain
29	1099	62.7	335	1	G2MSAB	Ig gamma-2a chain

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A>Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 95/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la:

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-93,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.4%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 7e-115;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 62

Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVVTVFSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

Db 61 GLYSLSVVTVFSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120

QY 123 FLFPPKPKDTLMSRTPVTCVVVDVSDPEDEPQFNWYVDGVEVHNAKTKPREEQFNSTY 182

Db 121 FLPPKPKDLMISRPVETCVVDVSDPEVQFVWYVDGVVHNAKTKPREEQFNSTY 180
Qy 183 RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKSKAGQPREPQVVTLPSPQSEMTK 242
Db 181 RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKSKAGQPREPQVVTLPSPQSEMTK 240
Qy 243 NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQEG 302
Db 241 NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQEG 300
Qy 303 NVFSCSVMHALHNYTKSLSLGK 329
Db 301 NVFSCSVMHALHNYTKSLSLGK 327

RESULT 2
GzHU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; PID:G6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Hofmann, T.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: Protein
A:Residues: 1-24, 'B', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOP>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidaci
red
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Fink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5792707
A:Contents: annotation; Sa, disulfide bonds

C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into li
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.5%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 3e-105;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

Qy 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Qy 63 GLYSLSVVTVFSSSLGKTITCNVDHKPSNTRKVDKVESKYGPPCPSCPAPELFGSPV 122
Db 61 GLYSLSVVTVFSSNFGTQITCNVDHKPSNTRKVDKVERKCCVCEPCPAPP-VAGPSV 119
Qy 123 FLFPKPKDLMISRPVETCVVDVSDPEVQFVWYVDGVVHNAKTKPREEQFNSTY 182
Db 120 FLFPKPKDLMISRPVETCVVDVSDPEVQFVWYVDGVVHNAKTKPREEQFNSTF 179
Qy 183 RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKSKAGQPREPQVVTLPSPQSEMTK 242
Db 180 RVSVSLFVLHODWLMNGKEYCKVSNKGLPSSIEKTKSKAGQPREPQVVTLPSPQSEMTK 239
Qy 243 NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQEG 302
Db 240 NOVSLTCLVKGFPSPDIAVWESNGQPNENYKTPPVLDSGDSGFFLYSLTLVDKSRWQEG 299
Qy 303 NVFSCSVMHALHNYTKSLSLGK 329
Db 300 NVFSCSVMHALHNYTKSLSLGK 326

RESULT 3
GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C:Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887

A:Molecule type: DNA
 A:Residues: 88-113:235-330 <TAk>
 A:Cross-references: EMBL:Z17370
 R:Cunningham, B.A.; Rutishauser, U.; Galli, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, Biochemistry 9, 3161-3170, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequence
 A:Reference number: A90563; MUID:71064024; PMID:5489771
 A:Contents: myeloma protein Eu
 A:Accession: B90563
 A:Molecule type: protein
 A:Residues: 1-96, 'R', 98-135 <CUN>
 A:Note: this sequence has the G1m(3) marker, 97-Arg
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M. Biochemistry 9, 3171-3181, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequence
 A:Reference number: A90564; MUID:71064025; PMID:5530842
 A:Contents: Eu
 A:Accession: A90564
 A:Molecule type: Protein
 A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'E', 242-268, 'E', 273-330 <SCH>
 A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
 R:Ponstingl, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), igen Primaerstruktur
 A:Reference number: A91668; MUID:77070269; PMID:826475
 A:Contents: myeloma protein Nie
 A:Accession: B91668
 A:Molecule type: protein
 A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-137, 'D', 139-238, 'D', 240, 'L', 242-268, 'E', 273-330 <SCH>
 A:Note: this sequence has the G1m(17) and G1m(1) markers
 R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 354, 713-747, 1983
 A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL
 A:Reference number: A91723; MUID:83289131; PMID:6884994
 A:Contents: myeloma protein KOL; disulfide bonds
 A:Accession: A91723
 A:Molecule type: protein
 A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH>
 A:Note: this sequence has the G1m(3) and G1m(non-1) markers
 R:Galli, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970
 A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide bonds
 A:Reference number: A90565; MUID:71064027; PMID:4923144
 A:Contents: annotation; disulfide bonds
 R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin
 A:Reference number: A91667; MUID:77070267; PMID:1002129
 A:Contents: annotation; disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG1
 A:Cross-references: GDB:120085; OMIM:147100
 A:Map position: 14q32.33-14q32.33
 A:Introns: 99/1; 114/1; 224/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into higher order oligomers.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM1>
 F;137-206/Domain: immunoglobulin homology <IM2>
 F;243-310/Domain: immunoglobulin homology <IM3>
 F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental
 F;103/Disulfide bonds: interchain (to light chain) #status experimental
 F;109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVVTVPPSSSLGKTTCNVNHNKPSNTKVDKRVESK---YGPSPSPCAPEFLGG 119
 Db 61 GLYSLSVVTVPPSSSLGKTTCNVNHNKPSNTKVDKRVESKCDKTHCTCPAPPELLGG 120
 QY 120 PSVFLPPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKREEQFN 179
 Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKREEQFN 180
 QY 180 STYRVSVTLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEE 239
 Db 181 STYRVSVTLTVLHODWLNKGYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSRDE 240
 QY 240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 299
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 300
 QY 300 QSGNVFSCSVNHEALHNHYTQKSLSLSPGK 329
 Db 301 QSGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
 RESULT 4
 A60764
 I: gamma-3 chain C region, form LAT - human
 C:Species: Homo sapiens (man)
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
 C:Accession: A60764
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
 A:Reference number: A60764; MUID:90007613; PMID:2571587
 A:Accession: A60764
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-377 <HUC>
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IM>
 Query Match 90.4%; Score 1585; DB 2; Length 377;
 Best Local Similarity 80.6%; Pred. No. 9.9e-104;
 Matches 304; Conservative 8; Mismatches 15; Indels 50; Gaps 1;
 QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSVVTVPPSSSLGKTTCNVNHNKPSNTKVDKRVESK---YGPSPSPCAPEFLGG 120
 Db 61 GLYSLSVVTVPPSSSLGKTTCNVNHNKPSNTKVDKRVESK---YGPSPSPCAPEFLGG 120
 QY 104 -----YGPSPSPCAPEFLGGPSVFLFPKPKDT 132
 Db 121 DTPPPCPSPSPCAPEFLGGPSVFLFPKPKDT 180
 QY 133 LMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKREEQFNSTYRVSVTLTVLH 192
 Db 181 LMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKREEQFNSTYRVSVTLTVLH 240
 QY 193 QDWLNKGYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 252
 Db 241 QDWLNKGYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK 300
 QY 253 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGNVFSVWME 312
 Db 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQGNVFSVWME 360
 QY 313 ALHNHYTQKSLSLSPGK 329
 Db 361 ALHNHYTQKSLSLSPGK 377

QY 3 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62

C:Genetics:
A:Gene: Igg2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 1289.5; DB 2; Length 328;
Best Local Similarity 72.0%; Pred. No. 4.2e-83;
Matches 237; Conservative 40; Mismatches 49; Indels 3; Gaps 2;
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 62
Db 1 AKTAPSVYPLAPCSRSTSGPNVALGCLASSYFPPEPTVWNSGALTSGVHTFPAVLQPS 60
QY 63 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESKYGPPCPSPAPPEFLGGPSV 122
Db 61 GLYSLSWTVTPASSLSKSYTCNVHPATITTKVDRVGITKTPCPICPACE-SFGPSV 119
QY 123 FLPPPKPOTLMISRTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTY 182
Db 120 FIFPPKPKDTLMISRTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTY 179
QY 183 RVSVLTVLHQQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQQEMTK 242
Db 180 RVSVLPIQHQQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPHAEELSR 239
QY 243 NOVSLTCLVKGFPSPDIKAVESNGQ--PENNYKTTTPPVLDSDGSPFLYRLTVDKSRWQ 300
Db 240 SKVSITCLVIGFYPPDIDVEMQNGQPEPEGNRYITPPQDQVDGTYFLYSKFSVDKASWQ 299
QY 301 EGNVFCNVVHEALHNHYTKSLSLGK 329
Db 300 GGGIFQCAVHEALHNHYTKSLSKTPGK 328

RESULT 7

I47160

Ig gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47160

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAAS2218.1; PID:G433126

C:Genetics:

A:Gene: Igg2b

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 73.2%; Score 1283.5; DB 2; Length 328;
Best Local Similarity 71.7%; Pred. No. 1.1e-82;
Matches 236; Conservative 39; Mismatches 51; Indels 3; Gaps 2;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 62

Db 1 AKTAPSVYPLAPCSRSTSGPNVALGCLASSYFPPEPTVWNSGALTSGVHTFPAVLQPS 60

QY 63 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESKYGPPCPSPAPPEFLGGPSV 122

Db 61 GLYSLSWTVTPASSLSKSYTCNVHPATITTKVDRVGITKTPCPICPACE-SFGPSV 119

QY 123 FLPPPKPOTLMISRTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTY 182

Db 120 FIFPPKPKDTLMISRTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTY 179

QY 183 RVSVLTVLHQQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQQEMTK 242

Db 180 RVSVLPIQHQQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPHAEELSR 239

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 1575; DB 2; Length 377;
Best Local Similarity 79.1%; Pred. No. 5e-103;
Matches 300; Conservative 12; Mismatches 15; Indels 50; Gaps 1;
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESK----- 103
Db 61 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESK----- 103

Query Match 89.8%; Score 1575; DB 2; Length 377;
Best Local Similarity 79.1%; Pred. No. 5e-103;
Matches 300; Conservative 12; Mismatches 15; Indels 50; Gaps 1;
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESK----- 103
Db 61 GLYSLSVWTVPSLSLGTITTCNVDPKSNKVDKRVESK----- 103

QY 104 -----YGPPCPSPAPPEFLGGPSVFPFPKPKDT 132

Db 121 DTPPPCPSPAPPEFLGGPSVFPFPKPKDT 132

QY 133 LMISTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTYRVSVLTVLH 192

Db 181 LMISTPEPTCVVVDVDSQSDPEVQFNWYVDGVVHNATKPREEQFNSTYRVSVLTVLH 240

QY 193 QDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQQEMTKNOVSLTCLVK 252

Db 241 QDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQQEMTKNOVSLTCLVK 300

QY 253 GYPSPDIKAVESNGQPEPNYKTTTPPVLDSDGSPFLYRLTVDKSRWQSGNVFSCVMHE 312

Db 301 GYPSPDIKAVESNGQPEPNYKTTTPPVLDSDGSPFLYRLTVDKSRWQSGNVFSCVMHE 360

QY 313 ALHNHYTKSLSLGK 329

Db 361 ALHNHYTKSLSLGK 377

RESULT 6

I47159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C:Accession: I47159

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine Igg identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47159

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAAS2217.1; PID:G433124

QY 243 NOVSLTCLVKGFPSPIAVESNGO--PENNYKTTTPVLDSGSPFLYSRLTYDKSRWQ 300
:
Db 240 SKVSIPTCLVIGFYPPDIDVEWQRNGQPPEGNRYRTTPQQDVDTGYFLYSKFSDKASWQ 299

QY 301 EGNVFSCSVNHEALHNHYTKSLSLGGK 329
:
Db 300 GGGIFCAVNHEALHNHYTKSISKTPGK 328

RESULT 8
I47161
Ig gamma 3 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RAC>
A;Cross-references: EMBL:U003781; NID:g433127; PIDN:AAA52219.1; PID:g433128
C;Genetics:
A;Gene: IgG3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 1264.5; DB 2; Length 328;
Best Local Similarity 70.8%; Pred. No. 2.4e-81;
Matches 233; Conservative 39; Mismatches 54; Indels 3; Gaps 2;

QY 3 ASTKGSPVPPLAPCSRSTSESTAALCLKVDYEPPEVTYVSWNSGALTSGVHTFPAYLQSS 62
:
Db 1 APTAPSVLPAPCGRDTSQPNVALGLASSYPPEVTMTWSGALTSGVHTFPAYLQPS 60

QY 63 GLYSLSGWTVTPSSSLGTITYTCNVDPKPSNTKVDRKVESKYGPCCPAPDFLGGPSV 122
:
Db 61 GLYSLSGWTVTPASSLSKKSYTCNVNHPATTTKVDRGVTKTFPCGPCI-
VAGPSV 119

QY 123 FLFPPPKXOTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGEVHNNAKTPREEQNSTY 182
:
Db 120 FIETPPPKXOTLMISQTPEVTCVVVDVSKEHAIEYQFSWYVDGEVHNAETPRKEEQENSTY 179

QY 183 RVVSVLTIVLHDWLNGEKYKCVSNKGLPSSIEKTIKAKGPREPOVQVTLPPSQEWMK 242
:
Db 180 RVVSVLIPTQHDDWLKGEFKCKVNNVDLPAPITRTSKAIGQSRREPQVTLPPABELSR 239

QY 243 NOVSLTCLVKGFPSPIAVESNGO--PENNYKTTTPVLDSGSPFLYSRLTYDKSRWQ 300
:
Db 240 SKVTVTCLVIGFYPPDIHVWEKNSGQPPEGNRYRTTPQQDVDTGYFLYSKLAVDKARWD 299

QY 301 EGNVFSCSVNHEALHNHYTKSLSLGGK 329
:
Db 300 HGFTFCAVNHEALHNHYTKSISKTPGK 328

RESULT 9
I47158
Ig gamma 1 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47158
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47158
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RAC>

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell, A;Reference number: A94416
 A;Accession: A94416
 A;Molecule type: protein
 A;Residues: 129-131;155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 'A';Note: this has the e15 allotypic marker, 185-Ala
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 18
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F;20-82/Domain: immunoglobulin homology <IM1>
 F;130-199/Domain: immunoglobulin homology <IM2>
 F;236-303/Domain: immunoglobulin homology <IM3>
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.4%; Score 1199; DB 1; Length 323;
 Best Local Similarity 69.0%; Pred. No. 9e-77;
 Matches 225; Conservative 35; Mismatches 58; Indels 8; Gaps 3;

QY 6 KPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNVSGALTSGVHTFPAVLQSSGLY 65
 Db 4 KAPSVFPPLAPCGDTPSSVTILGCLVKGYLPEPVTVTVNSGTLNGVTRTPPSVRQSSGLY 63

QY 66 SLSSVTVTPSSSLGKTITCNVDHKPSNTKVDKVESKYGPCC--PSCPAPFELGSPSVF 123
 Db 64 SLSSVTVTPSSS---QPVTCNVAHPATNTKVDKIVAPS---TCSKPTCPPELLGGPSVF 117

QY 124 LPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNSTYR 183
 Db 118 LPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNSTIR 177

QY 184 VYSLVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTKN 243
 Db 178 VYSLVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTKN 237

QY 244 QVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRWQEGN 303
 Db 238 VYSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRWQEGN 297

QY 304 VFCSCVMHEALHNHYTKQSLSLGK 329
 Db 298 VFCSCVMHEALHNHYTKQSLSLGK 323

RESULT 11
 S31459
 I;Gamma-1 chain - sheep (fragment)
 C;Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C;Accession: S31459
 R;Patri, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A;Reference number: S31459
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-472 <PAT>
 A;Cross-references: EMBL:X6797
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;277-346/Domain: immunoglobulin homology <IMM>

Query Match 68.4%; Score 1199; DB 2; Length 472;
 Best Local Similarity 67.5%; Pred. No. 1.5e-76;
 Matches 226; Conservative 34; Mismatches 63; Indels 12; Gaps 3;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNVSGALTSGVHTFPAVLQSS 62
 Db 142 ASTTPKPVPLSCCGDTPSSIVTLGCLVSSYMPPEVTVVNSGALTSGVHTFPAVLQSS 201

QY 63 GLYSLSSVTVTPSSSLGTTTYTCNVNDHKPSNTKVDKVESKYGP-PCSPCAPEFLGGPS 121
 Db 202 GLYSLSSVTVTPSSSLGTTTYTCNVNDHKPSNTKVDKVESKYGP-PCSPCAPEFLGGPS 260

QY 122 VLFPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNST 181
 Db 261 VLFPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNST 320

QY 182 YRVVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 241
 Db 321 YRVVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 380

QY 242 KNQVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRW 299
 Db 381 KSTVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRW 440

QY 117 LGGPSVFLPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREE 176
 Db 258 PGGPSVFLPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREE 317

QY 177 QNSYRVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 236
 Db 318 QNSYRVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 377

QY 237 QEMTKNQVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTV 294
 Db 378 QEELSKSTLSVTCLVTFGVFDYIAVEWQKNGQPESEDKYGTTSQDADGSEFFLYSLRLV 437

QY 295 DKSRWQEGNVPSCVMHEALHNHYTKQSLSLGK 329
 Db 438 DKSRWQEGNVPSCVMHEALHNHYTKQSLSLGK 472

RESULT 12
 S22080
 I;Gamma-1 chain precursor (B/WT 4A.17, H5, A5) - bovine
 N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S22080; S06610; A31303
 R;Sanders, P.G.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S22080
 A;Accession: S22080
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-470 <SAN>
 A;Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440
 R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
 Mol. Immunol. 26, 841-850, 1989
 A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gam
 A;Reference number: S06610; MUID:90097956; PMID:2513487
 A;Accession: S06610
 A;Molecule type: DNA
 A;Residues: 142-470 <SYM>
 A;Cross-references: EMBL:X16701
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Gene: Ig CH gamma-1
 A;Introns: 98/1; 111/1; 221/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
 F;161-225/Domain: immunoglobulin homology <IMM>
 F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.6%; Score 1185; DB 2; Length 470;
 Best Local Similarity 67.6%; Pred. No. 1.4e-75;
 Matches 223; Conservative 35; Mismatches 68; Indels 4; Gaps 3;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNVSGALTSGVHTFPAVLQSS 62
 Db 142 ASTTPKPVPLSCCGDTPSSIVTLGCLVSSYMPPEVTVVNSGALTSGVHTFPAVLQSS 201

QY 63 GLYSLSSVTVTPSSSLGTTTYTCNVNDHKPSNTKVDKVESKYGP-PCSPCAPEFLGGPS 121
 Db 202 GLYSLSSVTVTPSSSLGTTTYTCNVNDHKPSNTKVDKVESKYGP-PCSPCAPEFLGGPS 260

QY 122 VLFPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNST 181
 Db 261 VLFPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNST 320

QY 182 YRVVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 241
 Db 321 YRVVSVTLVHQLDNLNGKEYCKVSKNGKLPSSIEKTIKAKGQPREPQVYVTPPSPQEMTK 380

QY 242 KNQVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRW 299
 Db 381 KSTVSLTCLVKGFYPSDIAEVWESNGQPNYKTTTPVLDSDGSEFFLYSLRTVVDKSRW 440

```
QY 300 QEGNVFSCVMHEALHNHYTKSLSLKG 329
DB 441 QEGDVTTCVVMHEALHNHYTKSLSACK 470

RESULT 13
G2GP
IG gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence revision 07-May-1981 #text change 16-Jul-1999
C:Accession: A94553; A90352; A90359; A90384; A90385; A0151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein
A:Residues: 1-3 <TR>
R:Birstein, B.K.; Huseain, O.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A:Reference number: A90352; MUID:71058471; PMID:5538606
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BR>
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A:Reference number: A90359; MUID:71058486; PMID:5538616
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133;312-329 <TR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TR>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR>
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
Chain disulfide bonds. In some cases, such as IGA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
P:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:248-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Aen) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 66.0%; Score 1158; DB 1; Length 329;
Best Local Similarity 67.3%; Pred. No. 6.9e-74;
Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 4;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGLCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
DB 2 ARTTAPSVFPLAASCVDTSSTGSGMTGLCLVKGYFPEPTVKWNSGALTSGVHTFPAVLQ-S 60

Query Match 65.4%; Score 1147; DB 2; Length 308;
Best Local Similarity 69.1%; Pred. No. 3.7e-73;
Matches 215; Conservative 33; Mismatches 51; Indels 12; Gaps 3;

QY 27 LGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGCTFTCN 86
DB 2 LGCLVSSYMPPEPTVSNVNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGCTFTCN 61

QY 87 VDHKPSNTKVDKRVESKYGPCCPS-----CPAPEFLGGPSVFLPPKPKDTLMISRTPE 140
DB 62 VAHPASSTKVDKRV-----PCPPDPCKHCRCPPELPGGPSVFFPPKPKDTLTISGTPE 117

QY 141 VTCVVDVSDPEQVQFNWYVDGVEVHNATKPREOFNSTYRVVSVLTVLHQDWLNGKE 200
DB 118 VTCVVDVSDPEQVQFNWYVDGVEVHNATKPREOFNSTYRVVSVLTVLHQDWLNGKE 177

QY 201 YKCKYKNKGLSSSTKTKTSKAGQPREPQVYTLPPSQEEMTKNOVSLTCLVKGFVPSDIA 260
DB 178 FCKCKVNEALPAPIVTRISRTKQAREPQVYTLPPSQEELSKSLVSLTCLVTGFPDYIA 237

QY 261 VEWESNGQP--ENNYKTTPTFPVLDSDGSEFFLYSRITVDSKRWQEGNVFSCSMHEALHNHY 318
DB 238 VEWKNGQPESGDKYTTTSOLDADGSEFFLYSRITVDSKRWQEGNVFSCSMHEALHNHY 297

QY 319 TQKSLSLSGK 329
DB 298 TQKSLSKPFGK 308

RESULT 15
S69339
IG heavy chain V region precursor - human
C:Species: Homo sapiens (man)
```

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C/Accession: S69339; S72664
R/Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A/Reference number: S69339; PMID:7744049
A/Accession: S69339
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-374 <KHA>
A/Cross-references: EMBL:X81695
R/Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A/Reference number: S72664
A/Accession: S72664
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-140, 'C', 142-374 <KH2>
A/Cross-references: EMBL:X81695
C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 65.2%; Score 1143; DB 2; Length 374;
Best Local Similarity 76.4%; Pred. No. 9.1e-73;
Matches 220; Conservative 9; Mismatches 15; Indels 44; Gaps 3;

Qy	42	SWNSGALTSGVHTFPVAVLOSSGLYSLSVTVFSSSLGTYKTYTCNVDRHKPSNTKYDKRVE	101
Db	131	SWGQGT-----VTYSS-----EPKCDKTH-----	151
Qy	102	SKYGPCPCPAPEFLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNMYV	161
Db	152	-----TCPPCPAPELIGGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYV	206
Qy	162	DGVEVHNAKTPREDFNSTYRVSVLTVLHQDWLNGKYKCKVSNKGLPSSIEKTIISKA	221
Db	207	DGVEVHNAKTPREDFNSTYRVSVLTVLHQDWLNGKYKCKVSNKGLPSSIEKTIISKA	266
Qy	222	KGPREPQVYTLPPSOEEMTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPPVLD	281
Db	267	KGPREPQVYTLPPSREMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTTPPVLD	326
Qy	282	SDGSFFLYSLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLGK	329
Db	327	SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGX	374

Search completed: January 13, 2004, 12:44:43
Job time : 24.8489 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:19:34 ; Search time 14.3668 Seconds
(without alignments)
1076.912 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFASKGFSVPLAPCRST.....MHEALHNHYTKLSLSLKG 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1743	99.4	327	GC4_HUMAN	P01861 homo sapien
2	1605.5	91.5	326	GC4_HUMAN	P01859 homo sapien
3	1590.5	90.7	330	GCI_HUMAN	P01857 homo sapien
4	1199	68.4	323	GC_RABIT	P01870 oryctolagus
5	1158	66.0	329	GC2_CAVPO	P01862 cavia porce
6	1124	64.1	333	GC2_RAT	P20761 rattus norv
7	1118.5	63.8	326	GC1_RAT	P20759 rattus norv
8	1113.5	63.5	290	GC3_HUMAN	P01860 homo sapien
9	1108	63.2	329	GC2_RAT	P20762 rattus norv
10	1106.5	63.1	324	GCI_MOUSE	P01868 mus musculus
11	1106.5	63.1	330	GCAA_MOUSE	P01863 mus musculus
12	1101.5	62.8	393	GCIM_MOUSE	P01869 mus musculus
13	1101.5	62.8	399	GCAM_MOUSE	P01865 mus musculus
14	1099	62.7	335	GCAB_MOUSE	P01864 mus musculus
15	1098.5	62.6	329	GC3_MOUSE	P22436 mus musculus
16	1090.5	62.2	398	GC3M_MOUSE	P03987 mus musculus
17	1084.5	61.8	322	GCA_RAT	P20760 rattus norv
18	1054.5	60.1	336	GCB_MOUSE	P01866 mus musculus
19	1049.5	59.8	405	GCB_MOUSE	P01867 mus musculus
20	496	28.3	429	EPC_RAT	P01855 rattus norv
21	482.5	27.5	421	EPC_MOUSE	P06336 mus musculus
22	478.5	27.3	428	EPC_HUMAN	P01854 homo sapien
23	447.5	25.5	454	MUC_HUMAN	P01871 homo sapien
24	433.5	24.7	457	MUC_SUNMO	P20768 suncus muri
25	430.5	24.5	450	MUC_CANFA	P01874 canis famli
26	427.5	24.4	455	MUC_MOUSE	P01872 mus musculus
27	425.5	24.3	458	MUC_RABIT	P03988 oryctolagus
28	422	24.1	454	MUC_MSAU	P06337 mesocricetu
29	417.5	23.8	476	MUC_MOUSE	P01873 mus musculus
30	415.5	23.7	479	MUC_RABIT	P04221 oryctolagus
31	411.5	23.5	391	MUCB_HUMAN	P04220 homo sapien
32	393	22.4	353	ALC1_HUMAN	P01876 homo sapien
33	390.5	22.3	438	HVCS_HETFR	P23087 heterodontu

ALIGNMENTS

RESULT 1

ID	GC4_HUMAN	STANDARD	PRT	327 AA
AC	P01861			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	IG gamma-4 chain C region.			
GN	IGHG4			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83157104; PubMed=6299662;			
RA	Ellison J.W., Buxbaum J.N., Hood L.E.;			
RT	"Nucleotide sequence of a human immunoglobulin C gamma 4 gene."			
RN	DNA 1:11-18(1981).			
RN	[2]			
RP	SEQUENCE OF 1-30 AND 81-326.			
RX	MEDLINE=70207560; PubMed=4192699;			
RA	Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;			
RT	"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain."			
RT	Biochem. J. 117:33-47(1970).			
CC	-----			
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CC	-----			
DR	EMBL; K01316; AAB59394.1; ALT_INIT.			
DR	PIR; A90933; G4HU.			
DR	PDB; 1AQO; 16-SEP-98.			
DR	Genew; HGNC:5528; IGHG4.			
DR	MM; 147130; .			
DR	GO; 0005624; Cmembrane fraction; NAS.			
DR	GO; 0003823; F antigen binding activity; TAS.			
DR	GO; 0006955; P immune response; NAS.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG_c1.			
DR	InterPro; IPR003006; IG_MHC.			
DR	Pfam; PF00047; ig; 3.			
DR	SMART; SM00407; IGC1; 2.			
DR	PROSITE; PS00835; IG_LIKE; 3.			
DR	PROSITE; PS00290; IG_MHC; 2.			
DR	Immunoglobulin domain; Immunoglobulin C region; 3D-structure.			
FT	NON TER 1 98			
FT	DOMAIN 1 98			
FT	CH1.			
FT	99 110			
FT	HINGE.			
FT	111 220			
FT	CH2.			
FT	221 327			
FT	CH3.			

P20758 gorilla gor
P23085 heterodontu
P01877 homo sapien
P23088 heterodontu
P23084 heterodontu
P23086 heterodontu
P01878 mus musculu
P01875 gallus gall
P01879 oryctolagus
P23735 ictalurus p
P01880 homo sapien
P97797 m protein-t

FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 141 201

FT DISULFID 247 305

SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 99.4%; Score 1743; DB 1; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.2e-123; Indels 0; Gaps 0;

Matches 327; Conservative 0; Mismatches 0;

Qy 3 ASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPAPVLQSS 62

Db 1 ASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPAPVLQSS 60

Qy 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGPPSV 122

Db 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSPCAPPEFLGPPSV 120

Qy 123 FLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNKATKPREEQNSTY 182

Db 121 FLPPPKPDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYDGVVHNKATKPREEQNSTY 180

Qy 183 RVSVLTIVLHODWLNKGYKCKSNKGLPSIEKTIISKAKGQREPOVYTLPPSQEMTK 242

Db 181 RVSVLTIVLHODWLNKGYKCKSNKGLPSIEKTIISKAKGQREPOVYTLPPSQEMTK 240

Qy 243 NOVSLTCLVKGFYPSDIAVENSQGPENNYKTTTPVLDSDGFFLYSLRTVTDKSRWQEG 302

Db 241 NOVSLTCLVKGFYPSDIAVENSQGPENNYKTTTPVLDSDGFFLYSLRTVTDKSRWQEG 300

Qy 303 NVFSCSVMEALHNHYTKSLSLSLGK 329

Db 301 NVFSCSVMEALHNHYTKSLSLSLGK 327

RESULT 2

GC2_HUMAN

ID GC2_HUMAN STANDARD; PRT; 326 AA.

AC P01859;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE IG gamma-2 chain C region.

GN IGHG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE OF 2-326 FROM N.A.

RX MEDLINE=82197621; PubMed=6804948;

RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma

RT heavy chain constant region genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RN [2]

RP SEQUENCE OF 88-115 FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=83001943; PubMed=6811139;

RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;

RT "Structure of human immunoglobulin gamma genes: implications for

RT evolution of a gene family.";

RL Cell 29:671-679(1982).

RN [3]

RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=84235992; PubMed=6329676;

RA Krawinkel U., Rabbits T.H.;

RT "Comparison of the hinge-coding segments in human immunoglobulin gamma

RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass

RT genes.";

EMBO J. 1:403-407(1982).

[4]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

RX MEDLINE=81007873; PubMed=6774012;

RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic,

RT evolutionary, and functional implications.";

RL J. Immunol. 125:1048-1054(1980).

[5]

RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).

RX MEDLINE=80001357; PubMed=113060;

RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region

RT domains of a human IgG2 myeloma protein.";

RL Can. J. Biochem. 57:758-767(1979).

[6]

RP SEQUENCE OF 238-275 (ZIE).

RX MEDLINE=80114419; PubMed=118920;

RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human

RT immunoglobulin gamma chains.";

RL Mol. Immunol. 16:923-925(1979).

[7]

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).

RX Hofmann T., Parr D.M.;

RL Submitted (MAR-1980) to the PIR data bank.

[8]

RP SEQUENCE OF 1-121 (DOT).

RX MEDLINE=95255298; PubMed=7737190;

RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver P., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal

RT immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).

[9]

RP DISULFIDE BONDS.

RX MEDLINE=72033500; PubMed=4940472;

RA Milstein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";

RL Biochem. J. 121:217-225(1971).

[10]

RP DISULFIDE BONDS.

RX MEDLINE=69064124; PubMed=5782707;

RA Frangione B., Milstein C., Pink J.R.L.;

RT "Structural studies of immunoglobulin G.";

RL Nature 221:145-148(1969).

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DR EMBL; J00230; AAB59393.1; ..

DR PIR; A93906; G2HU

DR HSSP; P01857; 1FC1

DR Genew; HGNC:5526; IGHG2.

DR TIM; 147110; ..

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003823; F:antigen binding activity; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG_c1

DR InterPro; IPR003006; IG_MHC.

DR Pfam; PF00047; IG; 3.

DR SMART; SM00407; IGH1; 2.

DR PROSITE; PS00835; IG-LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON_TER 1 1

FT DOMAIN 99 110

FT CH1.

FT HINGE.


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FT DOMAIN 111 219
FT DOMAIN 220 326
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 91.5%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 2.4e-113;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 3 ASTKGSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVPSSTLGTTCNVDPKPSNTKVDKRVESKYGPPCPSPAPPEFLGGPSV 122
DB 61 GLYSLSVVTVPSSTLGTTCNVDPKPSNTKVDKRVESKYGPPCPSPAPPEFLGGPSV 119
QY 123 FLPPPKPDTLMISRPETVTCVVDVSDQEDPEVQFNWYDGVGVNNAKTPREEQFNSTY 182
DB 120 FLPPPKPDTLMISRPETVTCVVDVSHEDPEVQFNWYDGVGVNNAKTPREEQFNSTF 179
QY 183 RVSVLTVLHQLDWLNGKEYCKVSNKGLPSSIEKTIKSAKGPQRPQVYVTLPPSQEEMTK 242
DB 180 RVSVLTVLHQLDWLNGKEYCKVSNKGLPAPTEKTSKTKGQRPQVYVTLPPSQEEMTK 239
QY 243 NQVSLTCLVKGFPVSDIAVWESNGOPENNYKTPPEVLSDGSGFFLYSLRTVDKSRWQEG 302
DB 240 NQVSLTCLVKGFPVSDIAVWESNGOPENNYKTPPEVLSDGSGFFLYSLRTVDKSRWQEG 299
QY 303 NVFSCSVMEALHNYHTQKSLSLSLQK 329
DB 300 NVFSCSVMEALHNYHTQKSLSLSPGK 326

RESULT 3
GC1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 1g gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=62274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
(2)
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).

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RN SEQUENCE OF 136-329 (EU).
RP MEDLINE=71064025; PubMed=5530842;
RX Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
(4)
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
(5)
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
(6)
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
(7)
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
(8)
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER. 97-K, & THE
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
CC MARKER & THE GIM (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35, 116, 198, 269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198, 267&272.
CC
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CC
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT.
CC PIR; A93433; GHU.
CC PDB; 1FC1; 15-JUL-92.
CC PDB; 1FC2; 15-JUL-92.
CC PDB; 1AU7; 12-NOV-97.
CC PDB; 1D5B; 09-FEB-00.
CC
CC DR
CC DR
CC DR
CC DR
CC DR

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FT NON TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 202
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 66.04; Score 1158; DB 1; Length 329;
Best Local Similarity 67.3%; Pred. No. 8.7e-80;
Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 4;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 2 ARTTAPSVFPLAASCVDTSGMWTLGCLVKGYFPEPTVWNSGALTSGVHTFPAVLQ-S 60

QY 63 GLYSLSVVTVFPSSSLGKTCTYCNVDHKPSNTKVDKRVESKYGP-----PCPCPAPEFL 117
DB 61 GLYSLSMTVFPSS-----QKATCNVAHPASSTKVDKTVETPTZPBPCCTCPKCPPENL 116

QY 118 GGPVSFVFPKPKOTLMSRTPEVTCVVDVSDDEPQVFNWYDGVGVENAKTKGREEQ 177
DB 117 GGPVSFVFPKPKOTLMSRTPEVTCVVDVSDDEPQVFNWYDGVGVENAKTKGREEQ 176

QY 178 FNSYRVVSVLTVLHQDLWNGKEYCKVSKNGLPSSIEKTSISKAGQPRPQVYTLPPSQ 237
DB 177 YNTFRVESVLPPIQHQLWLRGKEFKCKVYKALPAPTEKTSISKAGAPRPQVYTLPPSR 236

QY 238 EEMTKQVSLCLVKGFPSPDIWVESNGOP--ENNYKTPPVLDSGSGFFLYSLTVD 295
DB 237 DELSKSKVSVTCLINFFPADIHVEWASNRVFPVSEKYEKNTPTIEDADGSIYLYSKLTV 296

QY 296 KSRWQEGNVFSCVMHEALHNHYTKQSLSLG 328
DB 297 KSNWQGVTVTCVVMHEALHNHYTKQSLSLG 329
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RESULT 6
GCB_RAT ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1 1
FT DOMAIN 6 96 IG-LIKE 1.
FT DOMAIN 124 223 IG-LIKE 2.
FT DOMAIN 232 328 IG-LIKE 3.
FT
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FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 64.1%; Score 1124; DB 1; Length 333;
Best Local Similarity 62.8%; Pred. No. 3.1e-77;
Matches 211; Conservative 46; Mismatches 67; Indels 12; Gaps 3;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 AQTAPSVFPLAPGCGDTTSTVTGLVKGYFPEPTVWNSGALTSDVHTFPAVLQ-S 59

QY 63 GLYSLSVVTVFPSSSLGKTCTYCNVDHKPSNTKVDKRVESKYG-----PPCPCPA 113
DB 60 GLYTITSSVT--SSTWPSQVTCNVAHPASSTKVDKVERNGGIGHKCTCPTCHKCPV 117

QY 114 PFLGPGSVFPLPFPKPKOTLMSRTPEVTCVVDVSDDEPQVFNWYDGVGVENAKTKP 173
DB 118 PELLGPGSVFPLPFPKPKOTLMSRTPEVTCVVDVSDDEPQVFNWYDGVGVENAKTKP 177

QY 174 REEQNSTYRVSVLTVLHQDLWNGKEYCKVSKNGLPSSIEKTSISKAGQPRPQVYTL 233
DB 178 REEQNSTYRVSVLTVLHQDLWNGKEYCKVSKNGLPSSIEKTSISKAGQPRPQVYTL 237

QY 234 PPSQEMTKQVSLCLVKGFPSPDIWVESNGOPENNYKTPPVLDSGSGFFLYSLT 293
DB 238 GPTTQLTEQVSLTCLTSGFLPNDIGVETWSNGHIEKNYKNTPEVMDSDGSGFFMYSKLN 297

QY 294 VDKSRWQEGNVFSCVMHEALHNHYTKQSLSLG 329
DB 298 VERSRWDRAPVCSVVMHEALHNHYTKQSLSLG 333
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RESULT 7
GCB_RAT ID GCB_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Bruggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DOMAIN 98 112 CH1.
FT DOMAIN 113 219 HINGE.
FT DOMAIN 220 326 CH2.
FT DISULFID 27 82 CH3.
FT
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RT cloned in a bacterial plasmid.";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salser W.
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain.";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gamma chain.";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
 RL Biochem. J. 126:837-850(1972).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=Displayed;
 CC Note=May be the major isoform;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=External;
 CC -----
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 DR EMBL; V00793; CAA24172.1; -;
 DR EMBL; V00793; CAA24173.1; -;
 DR EMBL; V00793; CAA24174.1; -;
 DR EMBL; V00793; CAA24175.1; -;
 DR EMBL; V00795; CAA24176.1; -;
 DR PIR; A02159; GIMS.
 DR PDB; 1IGC; 03-JUN-95.
 DR GlycoSuiteDB; P01868; -;
 DR MGD; MGI:96446; Igh-4;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; immunoglobulin C region; Glycoprotein;
 FT Alternative splicing; 3D-structure.
 FT NON_TER 1
 FT DOMAIN 1 97
 FT DOMAIN 98 110 CH1.
 FT DOMAIN 111 217 HINGE.
 FT DOMAIN 218 324 CH2.
 FT DOMAIN 27 82 CH3.
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARSHVD 174 174 N-LINKED (GLCNAC. . .).
 FT /FTID=CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324
 FT CONFLICT 276 276 REMOVED POST-TRANSLATIONALLY.
 FT N -> D (IN REF. 3).

PT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
 Query Match 63.1%; Score 1106.5; DB 1; Length 324;
 Best Local Similarity 62.0%; Pred. No. 6.2e-76;
 Matches 204; Conservative 55; Mismatches 63; Indels 7; Gaps 4;
 QY 3 ASTKGSVPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 1 AKTTPSVYPLAPGSAATNSMVTGLCLVKGYFPEPTVTSWNSGALTSGVHTFPAVLQSD 60
 QY 63 GLYSLSVVTVPSSSLTGTYTCNVDDHKPSNTKVDKRVESK--YGPCCPSCPAPFELGGP 120
 DB 61 -LYLSSSVTVPSPPSPSTVTCNVVHASSTKVDKIVPRCGCKPC-ICTVPEV---S 115
 QY 121 SVLFPPPKPDTLMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREEQFNS 180
 DB 116 SVFIFFPKPKDVLITITLTPKVCVVVDISKDDPEVQFSWFDVDDVEVHTAQTQPREEQFNS 175
 QY 181 TVAVSVLTVLHODWLNKGYCKYKNKGLPSIEKTIISKAKGQPREPOVYITLPPSQEEM 240
 DB 176 TFRSVSELPIMHQDWLNGKEFKRVNSAAPPAPIEKTIISKTRKRPAPQVYITIPPEQEM 235
 QY 241 TRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSLRTVDKSRMQ 300
 DB 236 AKDKVSLTCVITDFPEDITVEWQNGQPAENYKNTQPIIMNTNGSVFVYSLKNVQKSNWE 295
 QY 301 EGNVFSCSVMHEALHNHYTQKSLSLGLK 329
 DB 296 AGNTFTCSVLEGLHNHHTKLSHSPGK 324
 RESULT 11
 GCAA_MOUSE
 ID GCAA_MOUSE STANDARD; PRT; 330 AA.
 AC P01863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region, A allele.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81076554; PubMed=6777755;
 RA Sikorav J.-L., Auffray C., Rougeon F.;
 RT "Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
 RL Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81198976; PubMed=6262729;
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
 RL Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81223894; PubMed=6787604;
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE=74175517; PubMed=4831970;
 RA Bourgeois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-acid sequence of the Fc fragment. Implications

RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).

RN (5)
RX DISULFIDE BONDS.
RA MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
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DR EMBL; V00798; CAA24172.1; -;
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MWU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 63.1%; Score 1106.5; DB 1; Length 330;
Best local Similarity 63.0%; Pred. No. 6.3e-76;
Matches 209; Conservative 47; Mismatches 69; Indels 7; Gaps 4;
QY 3 ASTKGPSVFPPLAPCSRSTSEALGLVVDYFPEPVTVMNSGALTSGVHTTFFPAVLQSS 62
Db 1 AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYPPEPVTLTWNSGSLSGVHTTFFPAVLQSD 60
QY 63 GLYSLSVVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGP---PCP--SCPAPPEFL 117
Db 61 -LYTLSSSVTVTSSTPSQSCITCNVAHPASSTKVDKKIEPR-GPTIKPCPKCPAPNLL 118
QY 118 GGPSVFLPPEPKDFTLMSIRPTEVTCVVVDYSDPEVQFNWYDGVENNAKTKPREEQ 177
Db 119 GGPSVFIIPPKTKDVLMLSLSPITCVVDYSDPEVQFNWYDGVENNAKTKPREEQ 178
QY 178 FNSTVRVSVTLVTHQDMLNGKEYCKYKSNKGLPSSIEKTKISKAKGPRPQVYTLPPSQ 237
Db 179 YNSTLRVVSALPIQHODWMSGKEFKKVNKDLPAPIERTISKPKGSVRAPQVYTLPPPE 238
QY 238 EEMTKNOVSLTCLVKGFPSPDIADWESNGQPNKYKTPPVLDSDGSFFLYSLRTYDKS 297
Db 239 EEMTKQVTLTCWVDFPEDIYEWNTNGKTELKNTPEVLDSDGSFYFMISKRLVEKK 298
QY 298 RMQEGNVFSCSYMHEALNHHYTKSLSLSLGK 329
Db 299 NWVERNSYSCSVVHGLNHHHTKFSRTPGK 330

RESULT 12
GCIM_MOUSE STANDARD; PRT; 393 AA.
ID GCIM_MOUSE
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing, Named isoforms=2;
CC Name-Membrane-bound;
CC ISOID=P01869-1; Sequence=Displayed;
CC Name=Secreted;
CC ISOID=P01868-1; Sequence=External;
CC Note-May be the major isoform;
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; V00793; CAA24172.1; -;
DR EMBL; V00793; CAA24173.1; -;
DR EMBL; V00793; CAA24174.1; -;
DR PIR; B02159; GIMSM.
DR PDB; 15C8; 23-MAR-99.
DR PDB; 1A86; 18-MAR-98.
DR PDB; 1CL7; 12-JAN-00.
DR PDB; 1F11; 06-FEB-01.
DR PDB; 1F58; 29-DEC-99.
DR PDB; 1KCS; 24-JUL-02.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.


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DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IgC1; 2.  
DR PROSITE; PS00835; IG_LIKE; 3.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing; Transmembrane; 3D-structure.  
FT NON_TER 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 110 HINGE.  
FT DOMAIN 111 217 CH2.  
FT DOMAIN 218 324 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102  
FT DISULFID 104 104 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138 198  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
FT DISULFID 244 302  
FT TRANSMEM 340 357  
FT DOMAIN 358 393 POTENTIAL.  
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;  
  
Query Match 62.8%; Score 1101.5; DB 1; Length 393;  
Best Local Similarity 61.9%; Pred. No. 1.9e-75;  
Matches 203; Conservative 55; Mismatches 63; Indels 7; Gaps 4;  
  
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPETVSMNSGALTSGVHTFPAVLQSS 62  
DB 1 AKTTSPVYPLAPGSAAGTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTFPAVLQSD 60  
QY 63 GLYSLSVVTVPSSSLGTYTCNVDPKPSNTKVDKRVESK--YGPSPCPAPFELGGP 120  
DB 61 -LYTSSSVTVPSRRPSETVTCNVAHPASSTKVDKIKVPRDCGCKPC-ICTVPEV--S 115  
QY 121 SVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEPEVQFNWYVDGVEVHNAKTKPREEQFN 180  
DB 116 SVFIFFPKPKDLTITLTPKVTCTVVDVSKDPEPEVQFSWFVDVVEVHTAQVQPREEQFN 175  
QY 181 TVRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQHEM 240  
DB 176 TFRSVSELPIMHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQHEM 235  
QY 241 TKNQVSLTCLVKGYFSPDAVFNESNGOPENNYKTTTPVLDSDGSEFPLYSLTVDKSRWQ 300  
DB 236 ADKQVSLTCLMIDFFEDITVENQWNGQPAENYKNTQIPIMNINGSFYVSKLVNPKSNWE 295  
QY 301 EGNVFSVSMHEALHNHYTQKSLSLGL 328  
DB 296 AGNTFTCSVLHGLENNHHTKRSLSHPG 323  
  
RESULT 13  
GCAM_MOUSE STANDARD; PRT; 399 AA.  
AC P01865;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ig gamma-2A chain C region, membrane-bound form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=6222190; PubMed=6283537;  
RA Yamawaki-kataoka Y., Nakai S., Miyata T., Honjo T.;  
RT "Nucleotide sequences of gene segments encoding membrane domains of
```

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immunoglobulin gamma chains.";  
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
-!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2;  
CC Name-Membrane-bound;  
CC IsoId=P01865-1; Sequence=Displayed;  
CC Name=Secreted;  
CC IsoId=P01864-1; Sequence=External;  
CC Note=Probably the major isoform;  
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; J00471; AAB59661.1; ALT_INIT.  
DR PIR; A02154; G2MSAM.  
DR PUB; LKES; 08-APR-98.  
DR PDB; LYEE; 15-OCT-97.  
DR MGD; MGI:96443; Igh-1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00407; IgC1; 2.  
DR PROSITE; PS00835; IG_LIKE; 3.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Transmembrane; Alternative splicing; 3D-structure; Repeat.  
FT NON_TER 1 1  
FT DOMAIN 6 98 IG-LIKE 1.  
FT DOMAIN 121 220 IG-LIKE 2.  
FT DOMAIN 229 325 IG-LIKE 3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT TRANSMEM 346 363 POTENTIAL.  
FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FE0 CRC64;  
  
Query Match 62.8%; Score 1101.5; DB 1; Length 399;  
Best Local Similarity 62.8%; Pred. No. 1.9e-75;  
Matches 208; Conservative 47; Mismatches 69; Indels 7; Gaps 4;  
  
QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPETVSMNSGALTSGVHTFPAVLQSS 62  
DB 1 AKTTAPSVYPLAPVCGDTTGSSSVTLGCLVKGYFPPETVLTWNSGSLSSGVHTFPAVLQSD 60  
QY 63 GLYSLSVVTVPSSSLGTYTCNVDPKPSNTKVDKRVESKYGP---PCP--SCPAPEL 117  
DB 61 -LYTSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKPCPCCKCPAPNLL 118  
QY 118 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDPEPEVQFNWYVDGVEVHNAKTKPREQ 177  
DB 119 GGPSVFIFFPKPKDVLMISLVITCVVDVSDPEPDVQISWFWNNVEVHTAQTHRED 178  
QY 178 FNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQ 237  
DB 179 YNSTLWVSGALPIQHODWMSGKEFKCKVNNKOLPAPIERTISKPKGSRAPQVYVLPPE 238  
QY 238 EEMTKNOVSLTCLVKGYFSPDAVFNESNGQENNYKTTTPVLDSDGSEFPLYSLTVDKS 297  
DB 239 EEMTKQVTLTCLMIDFFEDITVENQWNGQPAENYKNTQIPIMNINGSFYVSKLVNPK 298
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QY 298 RWQEGNVFSCVMHEALHNNHYTKSLSLG 328
      |||:|||||:|||||:|||||:|||||:
Db 299 NWVERNSYSCSVVHEGLNHHHTKSFRTPG 329

RESULT 14
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=82037861; PubMed=6170065;
RX Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
IG2aa and IG2ab alleles of the mouse.";
RL proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwers M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- SURCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 1% OF THE POSITIONS.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
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CC
CC EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MGAB.
DR PDB; 1BOG; 23-MAR-99.
DR PDB; 1HH6; 26-JAN-01.
DR PDB; 1HH9; 12-JAN-01.
DR PDB; 1HI6; 08-FEB-01.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW 3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
SQ

Query Match 62.7%; Score 1099; DB 1; Length 335;
Best Local Similarity 60.7%; Pred. No. 2.4e-75;
Matches 204; Conservative 53; Mismatches 69; Indels 10; Gaps 3;

QY 3 ASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
      |||:|||||:|||||:|||||:|||||:
Db 1 AKTTAPSVYPLVPVCGGTGSGVTLGCLVKGYFPEPTVTLTSWNSGSLSSGVHTFFALQ-S 59
      |||:|||||:|||||:|||||:|||||:
QY 63 GLYSLSVVTVPSLSLGTQTYTCNVNDHKPSNTKVDKRVESKY---GPPC-----PSCP 113
      |||:|||||:|||||:|||||:|||||:
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKIEPRVPTQNPCHQRVPVPCAA 119
      |||:|||||:|||||:|||||:|||||:
QY 114 REFLGSPSVFLPPPKPKDTLMISRPETVCVVVDVSDVQEDFVNVDYDGVENHAKTKP 173
      |||:|||||:|||||:|||||:|||||:
Db 120 PLLLGSPSVFIIPPKIKDVLMSLSPMTCCVVDDVSEDDPDVQISWVNNVEVHTAQQT 179
      |||:|||||:|||||:|||||:|||||:
QY 174 REEQFNSTYRVVSVTLVHLDWLNKGKCYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 233
      |||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTLRVVVALPIQHQMWSGKFEKCKVNNRALPSPIKTIKSPGVPRAPOQVYVL 239
      |||:|||||:|||||:|||||:|||||:
QY 234 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFYLSSRLT 293
      |||:|||||:|||||:|||||:|||||:
Db 240 PPAEMTKKFSFLTKMITGLPFAIADWTSNGRTEQNTATVLDSDGSFYFWYKSR 299
      |||:|||||:|||||:|||||:|||||:
QY 294 VDKSRWQEGNVFSCVMHEALHNNHYTKSLSLGK 329
      |||:|||||:|||||:|||||:|||||:
Db 300 VQKSTWERSGLFACSVVHEVLNHLTTKTSRSLGK 335
      |||:|||||:|||||:|||||:|||||:

RESULT 15
GC3 MOUSE STANDARD; PRT; 329 AA.
ID GC3_MOUSE
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 98 113 CH1.
FT DOMAIN 114 223 HINGE.
FT DOMAIN 114 223 HINGE.
```

```
FT DOMAIN 224 327 CH3
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 62.8%; Score 1098.5; DB 1; Length 329;
Best Local Similarity 61.8%; Pred. No. 2.5e-75;
Matches 204; Conservative 50; Mismatches 71; Indels 5; Gaps 2;

QY 4 STKGPSVEPLAPCSRSTSESTAALGCLVXDYPEEPVTVSMNSGALTSGVHTTTPAVLQSSG 63
Db :|||:|||||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 TTTAPSVYFLVPCSDTSSSVTLGCLVKGYPPEPVTVRWNYGALSSGVRTVSSVLQ-SG 59

QY 64 LYSLSVTVTPSSSLGTKTYTCNVDRHKPSNTKYDKRVESKY---GPPCPCPAPEFLQG 119
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
60 FYSLSLVTVPSSTWPSQVICNVAPASKTELKRIEPRIPKPSSTPPGSSCPPGNILGG 119

QY 120 PSYELPPPKPDLMISRTPEVTCVVVDVSDPEQDPEVQFNWYVDGVVHNATKPREQFN 179
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
120 PSVFIFFPKPKDALMISLTPKVTCCVVVDVSEDDPDVHVSFVFNKEVHTAMTQPREAQYN 179

QY 180 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSOEE 239
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
180 STFRVVSALPIQHQQWNRGKEPKCKVNNKALPAPIERTISKPKGRAQTPQVYTIIPPREQ 239

QY 240 MTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTPVLDSGDSFELYSLTVDKSRW 299
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
240 MSKKKVSILTCLVNTFFSEAISEVWEERNGELEDQYKNTPPILDSDGTFLYSLKLTVDTSW 299

QY 300 QEGNVPFSCSVMEALHNHVTOKSLSLSLGK 329
Db :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
300 LQGEITCSVMEALHNHHTQKNLSRSPCK 329
```

Search completed: January 13, 2004, 12:39:29
Job time : 14.3668 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 58.9039 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-100
Perfect score: 1754
Sequence: 1 EFASIKGSPVFPPLACSRST.....MEEALNHYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_protein.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvillus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	99.4	473	4 Q8TC63	Q8tc63 homo sapien
2	1590.5	90.7	471	4 Q8TC77	Q8tc77 homo sapien
3	1578	90.0	521	4 Q8N4Y9	Q8n4y9 homo sapien
4	1570	89.5	509	4 Q8NF17	Q8nf17 homo sapien
5	1217	69.4	337	6 Q9SM34	Q9sm34 equus caball
6	1139.5	65.0	701	4 Q9PQ88	Q9pq88 homo sapien
7	1122.5	64.0	469	11 Q8R3V9	Q8r3v9 mus musculu
8	1119.5	63.8	463	11 Q99LC4	Q99lc4 mus musculu
9	1115.5	63.6	437	11 Q9R1A4	Q9r1a4 mus musculu
10	1112	63.4	473	11 Q9D8L4	Q9d8l4 mus musculu
11	1097.5	62.6	468	11 Q99L31	Q99l31 mus musculu
12	1087.5	62.6	473	11 Q99L25	Q99l25 mus musculu
13	1055.5	60.2	473	11 Q91Z05	Q91z05 mus musculu
14	1055.5	60.2	474	11 Q8R3H6	Q8r3h6 mus musculu
15	450	25.7	597	4 Q9BU10	Q9bu10 homo sapien
16	450	25.7	597	4 Q9BQ88	Q9bq88 homo sapien

17	450	25.7	597	4	Q96BB9	Q96bb9 homo sapien
18	440	25.1	588	4	Q8WUX4	Q8wux4 homo sapien
19	440	25.1	613	4	Q96EY0	Q96ey0 homo sapien
20	440	25.1	613	4	Q8WUK1	Q8wuk1 homo sapien
21	440	25.1	614	4	Q96GA6	Q96ga6 homo sapien
22	440	25.1	618	4	Q96AA6	Q96aa6 homo sapien
23	417.5	23.8	613	11	Q8VCX7	Q8vcx7 mus musculu
24	409	23.3	278	11	Q921K1	Q921k1 mus musculu
25	402.5	22.9	375	4	Q9BSZ1	Q9bsz1 homo sapien
26	393	22.4	384	4	Q9UP60	Q9up60 homo sapien
27	393	22.4	493	4	Q8NCL6	Q8nc16 homo sapien
28	393	22.4	494	4	Q96K58	Q96k58 homo sapien
29	393	22.4	496	4	Q96KX8	Q96kx8 homo sapien
30	390	22.2	496	4	Q96DK0	Q96dk0 homo sapien
31	390	22.2	499	4	Q8NSK4	Q8nsk4 homo sapien
32	388	22.1	497	4	Q8WY24	Q8wy24 homo sapien
33	388	22.1	500	4	Q9BRV0	Q9brv0 homo sapien
34	383.5	21.9	416	4	Q9NPP6	Q9npp6 homo sapien
35	377.5	21.5	486	11	Q91Z07	Q91z07 mus musculu
36	377.5	21.5	487	11	Q99KA4	Q99ka4 mus musculu
37	376.5	21.5	426	11	Q9DCD9	Q9dcd9 mus musculu
38	360	20.5	684	13	Q90544	Q90544 ginglymosto
39	358	20.4	481	11	Q91WT3	Q91wt3 mus musculu
40	358	20.4	481	11	Q91WT1	Q91wt1 mus musculu
41	358	20.4	482	11	Q91X92	Q91x92 mus musculu
42	358	20.4	482	11	Q8K172	Q8k172 mus musculu
43	358	20.4	484	11	Q8VEA0	Q8vea0 mus musculu
44	358	20.4	488	11	Q91WR1	Q91wr1 mus musculu
45	358	20.4	488	11	Q8XOF2	Q8xof2 mus musculu

ALIGNMENTS

RESULT 1

Q8TC63 ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63; 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EXBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 99.4%; Score 1743; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 3.1e-150;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGSVPFLACSRSTSESTALCLVKDYPPPEVTYVSNWNGALTSVHTFPVQLQS 62
Db 147 ASTKGSVPFLACSRSTSESTALCLVKDYPPPEVTYVSNWNGALTSVHTFPVQLQS 206
Qy 63 GLYSLSSVTVTPSSSLGTXTYTCNVDPKPSNTKVDKRVESKYGPCCPFAPEFLGGPSV 122

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE FLJ00385 protein (Fragment).
GN FLJ00385.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE-Spleen.
RA Jikuya H., Takano J., Kikuro R., Nagase T., Ohara O.;
RT "The nucleotide sequence of a long cDNA clone isolated from human spleen."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK090464; BAC03445.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 2.
FT NON_TER 1
SQ SEQUENCE 509 AA; 56111 MW; 089498D80765863C CRC64;
Query Match 79.5%; Score 1570; DB 4; Length 509;
Best Local Similarity 79.9%; Pred. No. 2e-134;
Matches 299; Conservative 11; Mismatches 14; Indels 50; Gaps 1;
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 64 ASTKGPSVFPLAPCSRSTSGTALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 123
QY 63 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVESK----- 103
DB 124 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVESK----- 103
QY 104 -----YGPCPCSCPAPELFGPSVFLFPKPKDT 132
DB 184 DTPPCPCPCPKSCDTPPCPCPCPKSCDTPPCPCPAPELFGPSVFLFPKPKDT 243
QY 133 LMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREQFNSTYAVWSVLTVLH 192
DB 244 LMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREQFNSTYAVWSVLTVLH 303
QY 193 QDWLNGKEYCKVKNKGLPSSIEKTIISKAKGPPEQVYTLPPSQEEMTKNQVSLTCLVK 252
DB 304 QDWLNGKEYCKVKNKGLPAPLIEKTIISKAKGPPEQVYTLPPSQEEMTKNQVSLTCLVK 363
QY 253 GFYPDSIAVEWESNGQPNENNYKTTTPVLDSDGSFPLYSRLTVDKSRWQEGNVFSCVMHE 312
DB 364 GFYPDSIAVEWESNGQPNENNYKTTTPVLDSDGSFPLYSRLTVDKSRWQEGNVFSCVMHE 423
QY 313 ALHNYTKQSLSL 326
DB 424 ALHNYTKQSLSL 437
RESULT 5
Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).
GN IGHCL1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.

RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."
RT Immunobiology 199;105-119(1998).
RL EMBL; AJ300675; CAC44624.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 2.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
Query Match 69.4%; Score 1217; DB 6; Length 337;
Best Local Similarity 66.3%; Pred. No. 1.6e-102;
Matches 226; Conservative 46; Mismatches 51; Indels 18; Gaps 3;
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTTAPKVPALAPGCGTTSSTVAGCLVSGYFPEPKVSNWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGKTTCNVYDHPKSNKVDKRVESK-----SKYGPSPCS 110
DB 61 GFYSLSVMVTVFASWTSETYICNVVHAASNFVKDKRIEPIPDNHQKVKDMSK---CPK 116
QY 111 CPAPELFGPSVFLFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATK 170
DB 117 CPAPELFGPSVFLFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATK 176
QY 171 TKPREQFNSTYAVWSVLTVLHQDWLNGKEYCKVKNKGLPSSIEKTIISKAKGPPEQV 230
DB 177 TRPKPEQFNSTYAVWSVLTVLHQDWLNGKEYCKVKNKGLPSSIEKTIISKAKGPPEQV 236
QY 231 YLPPSQEEMTKNQVSLTCLVKGFPSDTAVWESNGQP--ENNYKTTTPVLDSDGSFPL 288
DB 237 YVLAPHDPDLSSKSVTCLVKDFYPPEINIEQWNGQPELTKYSTTQAQDSDGSYFL 296
QY 289 YSLTVDKSRWQEGNVFSCVMHEALHNYTKQSLSLSGK 329
DB 297 YSLVDNRWQCGTTCGVWHEALHNYTKQVSKNFGK 337
RESULT 6
Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Factor VII active site mutant immunofugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."
RT Proc Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RL -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC EMBL; AF272774; AAK58686.1; -
DR HSP; P00761; IAN1.
DR InterPro; IPR000152; Asx_hydroxyl.

```
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_III.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002383; GLA blood.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001254; Ser. protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00047; Ig_2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0110; EGFblood.
DR PRINTS: PRO0001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00407; IGc1; 1.
DR SMART: SM00020; Tryp_SPG; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU CARBOXYLATION; 1.
DR PROSITE: PS00835; IG LIKE; 2.
DR PROSITE: PS00290; IG MHC; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 946C6B42CC992F CRC64;

Query Match 65.0%; Score 1139.5; DB 4; Length 701;
Best Local Similarity 73.0%; Pred. No. 5.1e-95;
Matches 219; Conservative 17; Mismatches 33; Indels 31; Gaps 3;

QY 41 VSNWGSALTSG-----VHTFPAVLQSSGLYSSVVTPSSSLGTTKTCNVDH 89
DB 422 VSWGQCATVGHFVYTRVSQVIEWLQKLMSEPRFGVLLRAPFGSA---EPKSCDNT 478

QY 90 KPSNTKVDKRVRKSGYGPSPAPFLGSPVFLFPKPKDITLMISRTPEVTCVVVDVS 149
DB 479 -----TCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 521

QY 150 QEDPEVQFNWYDGVGVHNAKTKPREQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 209
DB 522 HEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 581

QY 210 LPSSTIEKTSKAGQPREPQVYTLPPSSEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 269
DB 582 LPAPEKTSKAGQPREPQVYTLPPSSEELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 641

QY 270 ENNYKTPPVLDSDGFFLYSLRTVDKSRWEGNWFVSCVMHEALHNNHYTKSLSLGGK 329
DB 642 ENNYKTPPVLDSDGFFLYSLRTVDKSRWQGNWFVSCVMHEALHNNHYTKSLSLSPGK 701

RESULT 7
Q8R3V9 ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC024405; AAH24405.1; -.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 64.0%; Score 1122.5; DB 11; Length 469;
Best Local Similarity 62.9%; Pred. No. 1e-93;
Matches 207; Conservative 53; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPEPLAPCSRSTSESTAALGCLVKDYPPEPTVWNSGALTSVHTFPAVLQSS 62
DB 146 AKTTPESVYPLAPGSAAGTNSMTGLCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSD 205

QY 63 GLYSLSVVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESK--YGPSPCPAPFLGSP 120
DB 206 -LYTLSSSVTPSSSTWPSQTVCNVAHPASSTKVDKIVPRDCGCKPC-ICTVPEV--S 260

QY 121 SVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNWYDGVGVHNAKTKPREQFNS 180
DB 261 SVFIPEPKPKDTLTITLTKVTCVVVDISKDDPEVQFQFVDFVDDVHTAQTAPREQFNS 320

QY 181 TVRVSVLTVLHQDWLNGKEYKCKVSNKGLPISIETISKAKGQPREPQVYTLPPSQEEM 240
DB 321 TFRSVSELPIMHQDWLNGKEYKCKRVNSAFAPIETISKTGRPKAPQVYTIIPPKKEQM 380

QY 241 TRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGFFLYSLRTVDKSRWQ 300
DB 381 AKDKVSLTCLMTDFPEPDITVEQWNGQPAENYKNTQPIMDTDSGYFVYVKLVQKSNWE 440

QY 301 EGNVFCSCVMHEALHNNHYTKSLSLGGK 329
DB 441 AGNTFTCSVLHGLNHNHTEKLSLSPGK 469

RESULT 8
Q99LC4 ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 1810060009 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; IGH-4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BEC30783 CRC64;

Query Match 63.8%; Score 1119.5; DB 11; Length 463;
RN [1]
```

Best Local Similarity 62.6%; Pred. No. 1.9e-93;
Matches 206; Conservative 54; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVVWNSGALTSGVHTFPAVLQSS 62
Db 140 AKTTPSVVPLAPGAAQNSMTLGLVKGYFPEPVVWNSGSLSSGVHTFPAVLQSD 199
QY 63 GLYSLSVVTVFSSSLGTYTCNVDHKPSNTKDKRVESK--YGPSPCPAPFELGGP 120
Db 200 -LYTLSSVTVFSSWPSSTVTCNVAHPASSTKVDKIVPRDCGKPC-ICTVEV---S 254
QY 121 SVFLPPPKDITLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKATKPREEQFNS 180
Db 255 SVFIFFPKPKDVTILITPKVTCVVVDISKDDPEVQFNFVDDVEVHTAQTQPREEQFNS 314
QY 181 TYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKQGPPEQVYITLPPSQEEM 240
Db 315 TFRSVSELPIMHQDWLNGKEYKCRVNSAAPPATIEKTIKTKGRPKAPQVYITLPPKQEQM 374
QY 241 TKQVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQ 300
Db 375 AKDKVSLTCMTITFFPEDITVEMQWNGQPAENYKNTQPIMDTDGSYFVYKLVNQKSNWE 434
QY 301 EGNVFCSCVMHEALHNHYTKSLSLGK 329
Db 435 AGNTFTCSVLHGLHNHTEKLSHSPGK 463

RESULT 9
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
DE Gammai heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv)."
RL Submitted (WAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; A152372; AAD40243.1; -;
DR FSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR SMART; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3E7D697C CRC64;

Query Match 63.6%; Score 1115.5; DB 11; Length 437;
Best Local Similarity 62.3%; Pred. No. 4.1e-93;
Matches 205; Conservative 55; Mismatches 62; Indels 7; Gaps 4;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVVWNSGALTSGVHTFPAVLQSS 62
Db 114 AKTTPSVVPLAPGAAQNSMTLGLVKGYFPEPVVWNSGSLSSGVHTFPAVLQSD 173
QY 63 GLYSLSVVTVFSSSLGTYTCNVDHKPSNTKDKRVESK--YGPSPCPAPFELGGP 120
Db 174 -LYTLSSVTVFSSWPSSTVTCNVAHPASSTKVDKIVPRDCGKPC-ICTVEV---S 228

QY 121 SVFLPPPKDITLMISRTPEVTCVVVDVSDPEVQFNWYVDGVVHNKATKPREEQFNS 180
Db 229 SVFIFFPKPKDVTILITPKVTCVVVDISKDDPEVQFNFVDDVEVHTAQTQPREEQFNS 288
QY 181 TYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKQGPPEQVYITLPPSQEEM 240
Db 289 TFRSVSELPIMHQDWLNGKEYKCRVNSAAPPATIEKTIKTKGRPKAPQVYITLPPKQEQM 348
QY 241 TKQVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQ 300
Db 349 AKDKVSLTCMTITFFPEDITVEMQWNGQPAENYKNTQPIMDTDGSYFVYKLVNQKSNWE 408
QY 301 EGNVFCSCVMHEALHNHYTKSLSLGK 329
Db 409 AGNTFTCSVLHGLHNHTEKLSHSPGK 437

RESULT 10
Q9D8L4
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Havaehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB29349.1; -;
DR FSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 63.4%; Score 1112; DB 11; Length 473;
Best Local Similarity 61.3%; Pred. No. 9.5e-93;
Matches 206; Conservative 53; Mismatches 67; Indels 10; Gaps 3;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVVWNSGALTSGVHTFPAVLQSS 62
Db 114 AKTTPSVVPLAPGAAQNSMTLGLVKGYFPEPVVWNSGSLSSGVHTFPAVLQSD 173
QY 63 GLYSLSVVTVFSSSLGTYTCNVHDPKPSNTKDKRVESK--YGPSPCPAPFELGGP 120
Db 174 -LYTLSSVTVFSSWPSSTVTCNVAHPASSTKVDKIVPRDCGKPC-ICTVEV---S 228


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Db 139 AKTAPSVYPLAPVCGGTTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTRPALLQ-S 197
Qy 63 GLYSLSVVTVPPSSSLGTTKVTTCNVVDHKPSNTKVDKRVESKYG-----PP---CPSCPA 113
Db 198 GLYTLSSSVTVTSNTWPSQTTCNVVAHPASSTKVDKIEPRVPTQNPCCPLKECPFCAA 257
Qy 114 PFLGGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSDDEPVEQFNWYVDGVEVHNAKTKP 173
Db 258 PDLGGSPVFFPPKIKDVLMLSLSPMTCCVVVDSEDDPDVQISWFWVNVVHTAQTTQT 317
Qy 174 REEQNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPOVYTL 233
Db 318 HREDYNTSLRVVSALPIQHDWMSGKEFKCKVNNKALPSPIEKTIISKRGFVRAPOVYVL 377
Qy 234 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 293
Db 378 PPAEMTKKQSFLTCXLTGTLPALIAVDWTSNGRTEQNTATVLDSDGSFYFMYSKLR 437
Qy 294 VDKRWQGNVFCSCVMHEALHNHYTQKSLSLGLK 329
Db 438 VOKSTWERSGLFACSVVHGLHNHLTTTKTISRSLGK 473

RESULT 11
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 62.6%; Score 1097.5; DB 11; Length 468;
Best Local Similarity 62.7%; Pred. No. 28-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 139 AKTAPSVYPLAPVCGGTTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTFPAVLQSD 198
Qy 63 GLYSLSVVTVPPSSSLGTTKVTTCNVVDHKPSNTKVDKRVESKYG---PCP---SCPAPEFL 117
Db 199 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 256
Qy 118 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDDEPVEQFNWYVDGVEVHNAKTKPREEQ 177
Db 257 GGPSVFIFFPKIKDVLMLSLSPMTCCVVVDSEDDPDVQISWFWVNVVHTAQTTQTHRED 316
Qy 178 FNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQ 237
Db 317 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPOVYVLPPE 376
Qy 238 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKS 297
Db 377 EEMTKQVLTLCNVTDMPEDIVVETWNNKGTALYKNTPEVLDSDGSFYFMYSKLRVKK 436

Query Match 62.6%; Score 1097.5; DB 11; Length 468;
Best Local Similarity 62.7%; Pred. No. 28-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVYPLAPVCGGTTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTFPAVLQSD 203
Qy 63 GLYSLSVVTVPPSSSLGTTKVTTCNVVDHKPSNTKVDKRVESKYG---PCP---SCPAPEFL 117
Db 204 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 261
Qy 118 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDDEPVEQFNWYVDGVEVHNAKTKPREEQ 177
Db 262 GGPSVFIFFPKIKDVLMLSLSPMTCCVVVDSEDDPDVQISWFWVNVVHTAQTTQTHRED 321
Qy 178 FNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQ 237
Db 322 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPOVYVLPPE 381
Qy 238 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKS 297
Db 382 EEMTKQVLTLCNVTDMPEDIVVETWNNKGTALYKNTPEVLDSDGSFYFMYSKLRVKK 441
Qy 298 RWQGNVFCSCVMHEALHNHYTQKSLSLGLK 329
Db 442 NWVERNSYSCSVVHGLHNHLTTKSPRTPGK 473

RESULT 13
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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Qy 298 RWQGNVFCSCVMHEALHNHYTQKSLSLGLK 329
Db 437 NWVERNSYSCSVVHGLHNHLTTKSPRTPGK 468

RESULT 12
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.6%; Score 1097.5; DB 11; Length 473;
Best Local Similarity 62.7%; Pred. No. 28-91;
Matches 208; Conservative 47; Mismatches 70; Indels 7; Gaps 4;

Qy 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPPVTVSMNSGALTSGVHTFPAVLQSS 62
Db 144 AKTAPSVYPLAPVCGGTTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTFPAVLQSD 203
Qy 63 GLYSLSVVTVPPSSSLGTTKVTTCNVVDHKPSNTKVDKRVESKYG---PCP---SCPAPEFL 117
Db 204 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKIEPR-GPTIKCPCKCPAPNLL 261
Qy 118 GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDDEPVEQFNWYVDGVEVHNAKTKPREEQ 177
Db 262 GGPSVFIFFPKIKDVLMLSLSPMTCCVVVDSEDDPDVQISWFWVNVVHTAQTTQTHRED 321
Qy 178 FNSTYRVSVLTVLHODWLNKKEYCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQ 237
Db 322 YNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPOVYVLPPE 381
Qy 238 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKS 297
Db 382 EEMTKQVLTLCNVTDMPEDIVVETWNNKGTALYKNTPEVLDSDGSFYFMYSKLRVKK 441
Qy 298 RWQGNVFCSCVMHEALHNHYTQKSLSLGLK 329
Db 442 NWVERNSYSCSVVHGLHNHLTTKSPRTPGK 473

RESULT 13
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010327; AAH10327.1; -.
 DR MGD; MGI:2144967; AU044919.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 60.2%; Score 1055.5; DB 11; Length 473;
 Best Local Similarity 59.5%; Pred. NO. 1.3e-87;
 Matches 201; Conservative 51; Mismatches 73; Indels 13; Gaps 4;
 QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPPVTVSWNSGALTSVHTFPAVLQSS 62
 DB 138 AKTTPSVYPLAPGCGDTTGSVTLGCLVKGYFPPESVTVWNSGSLSSVHTFPALLQ-S 196
 QY 63 GLYSLSVVTVPSSSLGTTTCNVDHKPSNTKVDKRVESKYGP-----PCP-----SC 111
 DB 197 GLYTSSSVTVPSSTWPSQTVTCSVAHPASSTVTDKLEPS-GPISTINPCPKCKECHK 255
 QY 112 PAPEFLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKT 171
 DB 256 PARNLEGGPSVFIPFNKIDVLMISLTPTKVTCTVVVDVSDPEVQFNWYVDGVEVHNAKT 315
 QY 172 KPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVY 231
 DB 316 QTHREDYNSTIRVVSALPPIQHCDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY 375
 QY 232 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGDSFFLYSR 291
 DB 376 ILPPPAEQSKRDVSLTCLVGFNPGDISVETNSNGTEENYKDTAPVLDSDGSFYFIYSK 435
 QY 292 LTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLGK 329
 DB 436 LDIKTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK 473

RESULT 14
 Q8R3H6 PRELIMINARY; PRT; 474 AA.
 AC Q8R3H6
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 51.7 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025447; AAH25447.1; -.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.

DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein_
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
 Query Match 60.2%; Score 1055.5; DB 11; Length 474;
 Best Local Similarity 59.5%; Pred. NO. 1.3e-87;
 Matches 201; Conservative 51; Mismatches 73; Indels 13; Gaps 4;
 QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPPVTVSWNSGALTSVHTFPAVLQSS 62
 DB 139 AKTTPSVYPLAPGCGDTTGSVTLGCLVKGYFPPESVTVWNSGSLSSVHTFPALLQ-S 197
 QY 63 GLYSLSVVTVPSSSLGTTTCNVDHKPSNTKVDKRVESKYGP-----PCP-----SC 111
 DB 198 GLYTSSSVTVPSSTWPSQTVTCSVAHPASSTVTDKLEPS-GPISTINPCPKCKECHK 256
 QY 112 PAPEFLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKT 171
 DB 257 PARNLEGGPSVFIPFNKIDVLMISLTPTKVTCTVVVDVSDPEVQFNWYVDGVEVHNAKT 316
 QY 172 KPREEQFNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVY 231
 DB 317 QTHREDYNSTIRVVSALPPIQHCDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY 376
 QY 232 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSGDSFFLYSR 291
 DB 377 ILPPPAEQSKRDVSLTCLVGFNPGDISVETNSNGTEENYKDTAPVLDSDGSFYFIYSK 436
 QY 292 LTVDKSRWQEGNVFSCVMHEALHNNHYTKSLSLGK 329
 DB 437 LDIKTSKWEKTSFSCNVRHEGLKNYLYLKTISRSPGK 474

RESULT 15
 Q9BU10 PRELIMINARY; PRT; 597 AA.
 AC Q9BU10
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002963; AAH02963.1; -.
 DR HSP; P01825; 7PAB.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 5.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; 3.
 KW Hypothetical protein_
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 25.7%; Score 450; DB 4; Length 597;
 Best Local Similarity 26.9%; Pred. NO. 2.6e-32;
 Matches 118; Conservative 71; Mismatches 132; Indels 118; Gaps 17;
 QY 4 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPPVTVSW-NSGALTSVHTFPAVLQ 60
 DB 146 SASAPLFLVLCNSGPSSTSSVAVGCLAQDLPDSITFSWKYKNSDSSIRGFFSVLR 205
 QY 61 SSGLYSLSSVTVPSSSL--GTKTY-TCNVDHKPSNTKVDKRV----- 100

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Db 206 -GGKYAATSQVLLPSKDVMOQGTDEHVCKVCH-PNGNK-EKNVPLPVIABLPPKVSFVP 262
QY 101 --ESKYGPSPS---CPAPEL-----GGPS---- 121
Db 263 PRDGFNGNPRKSLKICQATGSPRQIQVSWLREGKQVSGVTTDOVQAEAKESGPTTKY 322
QY 122 -----VFLPPPKPKDTLMIS 136
Db 323 TSTLTIKESDMLSQSMF*CRVDHRLTPOQNASSMCPVDDQTAIRVFAIPPS-FASIFLT 381
QY 137 RPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVJHODWL 196
Db 382 KSTKUTCLVTLTITVD-SVTISWTRQGEAVKTHNISESHPNATFSAVGEASICEDDWN 440
QY 197 NGKEYKCKVSNKGLPSSIEKTIISKAKQP-REPOVYTLPPSQEEMT-KNOVSLTCLVKGF 254
Db 441 SGERFTCTVHTDLPSPPLKQIISRPKGVALHRPDVYLLPPAREQLNLRGATITCLVTGF 500
QY 255 YPSDIWVESWNGQP--ENNYKTPPVL--SDGSFPLYSELTVDKSRWQEGNVFSCVM 310
Db 501 SPADVFOVMORGQPLSPEKYVTGAPMPEPQAGRYFAHSILTVSEEWNTGETYTTCVA 560
QY 311 HEALHNHYTQKSLSLGLK 329
Db 561 HEALPNRVTERIVDKSTCK 579
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Search completed: January 13, 2004, 12:43:11
Job time : 59.9039 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:18:44 ; Search time 76.7188 Seconds
(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754

Sequence: 1 EFATKGPSVFPLAPCRST.....MHEALNNHYTKLSLSLCK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	99.4	327	18 AAW37346	Immunoglobulin C-g
2	1743	99.4	327	23 AAM47859	Human Ig-G4 heavy
3	1743	99.4	327	24 AAE32630	Human immunoglobul
4	1743	99.4	327	24 AAE32918	Human immunoglobul
5	1743	99.4	329	20 AAW70801	Amino acid sequenc
6	1743	99.4	329	21 AAY2190	Human IGG1 C-gamma
7	1743	99.4	443	21 AAW13564	Humanised anti-I-s
8	1743	99.4	444	20 AAY31672	Human IGG4 chain C
9	1743	99.4	463	18 AAW14935	2A2 Human IGG4 exp

10	1743	99.4	463	18 AAW14932	Murine anti-porcine
11	1743	99.4	464	18 AAW14941	3F4 Human IGG4 exp
12	1743	99.4	464	18 AAW14938	Murine anti-porcine
13	1743	99.4	467	16 AAR80617	Anti-human IL-4 hu
14	1743	99.4	467	18 AAW14925	Human gamma-4 heavy
15	1743	99.4	468	13 AAR28808	pre-SA8 humanised
16	1738	99.1	450	24 ABP96294	4A5-3.1.1-B4 antib
17	1736	99.0	467	18 AAW14926	Human gamma-4E hea
18	1731	98.7	462	18 AAW14927	P-selectin ligand
19	1725	98.3	422	20 AAY29771	P-selectin ligand
20	1725	98.3	533	20 AAY29773	P-selectin ligand
21	1720	98.1	646	20 AAY29775	TP8-SG9 CDR-grafte
22	1716.5	97.9	447	18 AAW10232	Humanised 323/A3 (
23	1716	97.8	462	22 AAB72234	Humanised 323/A3 (
24	1710	97.5	462	22 AAB72229	Humanised 323/A3 (
25	1649.5	94.0	462	18 AAW14933	2A2 (Chimeric) hum
26	1649.5	94.0	462	18 AAW14934	2A2 (Chimeric) hum
27	1649.5	94.0	463	18 AAW14939	3F4 (Chimeric) hum
28	1649.5	94.0	463	18 AAW14940	3F4 (Chimeric) hum
29	1649.5	94.0	472	23 ABP51695	SG1.1-TPO heavy ch
30	1611.5	91.9	530	13 AAR26783	CD4-IgG2 chimeric
31	1611.5	91.9	530	21 AAY85080	CD4-IgG2 chimeric
32	1611.5	91.9	530	22 AAB80884	Human CD4-IgG2 chi
33	1611.5	91.9	530	22 AAB67323	CD4-IgG2 chimeric
34	1611.5	91.9	530	24 ABG71123	CD4-immunoglobulin
35	1607.5	91.6	442	22 AAB72230	Humanised 323/A3 (
36	1607.5	91.6	461	22 AAB72236	Humanised 323/A3 (
37	1605.5	91.5	326	22 AAE02643	Human immunoglobul
38	1605.5	91.5	326	23 ABG77148	Anti-IGF-IR consta
39	1605.5	91.5	326	23 ABG30462	Human anti-CD40 mo
40	1605.5	91.5	326	23 AAM47857	Human Ig-G2 heavy
41	1605.5	91.5	326	24 AAE32628	Human immunoglobul
42	1605.5	91.5	326	24 AAE32916	Human immunoglobul
43	1605.5	91.5	443	20 AAY31670	Human IGG3 chain C
44	1605.5	91.5	451	21 AAY93734	The heavy chain of
45	1605.5	91.5	462	21 AAB26884	Human immunoglobul

ALIGNMENTS

RESULT 1
AAW37346
ID AAW37346 standard; Protein; 327 AA.
XX
AAW37346;
AC
XX
DT 11-MAY-1998 (first entry)
XX
DE Immunoglobulin C-gamma-4 region.
XX
KW Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
KW gene amplification; immunotherapy; therapy; immunoglobulin;
KW C-gamma-4; constant region.
XX
OS Homo sapiens.
XX
PN WO9741244-A1.
XX
PD 06-NOV-1997.
XX
PF 25-APR-1997; 97WO-US07039.
XX
PR 06-DEC-1996; 96US-0761277.
PR 01-MAY-1996; 96US-0644664.
(GENI-) GENOTOPE CORP.
PI Denney DW;
XX
DR WPI; 1997-549743/50.
DR N-P8DB; AAT97189.
XX

PT Multivalent vaccine to treat B cell lymphoma or leukaemia -
 PT comprises at least 2 different recombinant variable regions of
 PT immunoglobulin molecules derived from B cell lymphoma cells
 XX
 XX
 PS Example 10; Page 126-127; 177pp; English.

XX This protein comprises an immunoglobulin (Ig) C-gamma-4 region.
 CC The invention provides a method for the production of tumour-
 CC specific Ig derived from a B-cell lymphoma patient. In the novel
 CC method, expression plasmids containing the patient's VH region(s)
 CC joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
 CC sequence and expression plasmids containing the patient's VL
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2
 CC (see AAT97191) sequence are cotransfected along with a selectable and
 CC amplifiable marker into a cell line (e.g. BMS147.G.1.4), and
 CC transfected cells are then subjected to selection and amplification.
 CC The method permits the production of a multivalent vaccine which
 CC reflects the degree of somatic variation found within the patient's
 CC tumour. These novel multivalent vaccines provide superior vaccines
 CC for the treatment of B-cell lymphoma.

XX SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 18; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2.1e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSSVTVTPSSSLGTITCNVDHKPNTKVDKRVESKYGPPCPSCPAPEFLGSPV 122
 DB 61 GLYSLSSVTVTPSSSLGTITCNVDHKPNTKVDKRVESKYGPPCPSCPAPEFLGSPV 120
 QY 123 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182
 DB 121 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 180
 QY 183 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
 DB 181 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
 QY 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
 DB 241 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 300
 QY 303 NVFSCSVNMEALHNHYTQKSLSLGLK 329
 DB 301 NVFSCSVNMEALHNHYTQKSLSLGLK 327

RESULT 2
 ID AAM47859
 AC AAM47859
 XX AAM47859 standard; Protein; 327 AA.
 DT 22-FEB-2002 (first entry)
 DE Human Ig-G4 heavy chain constant region amino acid sequence.
 XX Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.
 XX Homo sapiens.
 OS
 XX WO200183529-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 28-APR-2001; 2001WO-US13932.

XX 28-APR-2000; 2000US-200298P.
 PR (PLAN-) PLANET BIOTECHNOLOGY INC.
 XX Larrick JW, Wycoff KL;
 PI WPI; 2002-041481/05.
 DR N-PSDB; ABA05268.
 XX Immunoadhesin for treating human rhinovirus infection comprises
 PT chimeric intercellular adhesion molecule-1, and optionally a J chain
 PT and secretory component in association
 XX
 PT Disclosure; Fig 7; 138pp; English.

XX The invention relates to an immunoadhesin comprising:
 CC (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a
 CC rhinovirus receptor protein linked to at least a portion of an
 CC immunoglobulin heavy chain; and
 CC (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or uncoating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J
 CC chain increases the stability of the immunoadhesin in the mucosal
 CC environment. Production is significantly less expensive in plants than in
 CC animal cell culture and production in plants is safer for human use,
 CC since plants are not known to harbor any animal viruses. The present
 CC sequence is that of a human immunoglobulin protein sequence, useful to
 CC the invention.

XX SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 23; Length 327;
 Best Local Similarity 100.0%; Pred. No. 2.1e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
 DB 1 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 QY 63 GLYSLSSVTVTPSSSLGTITCNVDHKPNTKVDKRVESKYGPPCPSCPAPEFLGSPV 122
 DB 61 GLYSLSSVTVTPSSSLGTITCNVDHKPNTKVDKRVESKYGPPCPSCPAPEFLGSPV 120
 QY 123 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 182
 DB 121 FLPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNATKPREQFNSTY 180
 QY 183 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
 DB 181 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
 QY 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
 DB 241 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 300
 QY 303 NVFSCSVNMEALHNHYTQKSLSLGLK 329
 DB 301 NVFSCSVNMEALHNHYTQKSLSLGLK 327

RESULT 3
 AAE32630
 ID AAE32630 standard; Protein; 327 AA.

XX AAE32630;
AC 24-MAR-2003 (first entry)
DT Human immunoglobulin G4 (IgG4) heavy chain Fc region.
DE Human; immunogenic; therapy; immunoglobulin G4; IgG4.
XX Homo sapiens.
OS WO200279415-A2.
XX 10-OCT-2002.
PD 29-MAR-2002; 2002WO-US09650.
XX 30-MAR-2001; 2001US-280625P.
XX (LEXI-) LEXIGEN PHARM CORP.
XX Gillies SD;
XX WPI; 2003-111794/10.

XX Reducing the immunogenicity of a fusion protein by changing an amino
PT acid within the junction region spanning a fusion junction of a fusion
PT protein to reduce the ability of the candidate T-cell epitope to
PT interact with a T-cell receptor -
XX Disclosure; Page 53; 67pp; English.

XX The present invention relates to a method of reducing the immunogenicity
CC of a fusion protein. The method involves identifying a candidate T-cell
CC epitope within a junction region spanning a fusion junction of a fusion
CC protein and changing an amino acid within the junction region to reduce
CC the ability of the candidate T-cell epitope to interact with a T-cell
CC receptor. The method is useful for reducing the immunogenicity of fusion
CC proteins for use in therapy. The present sequence is human immunoglobulin
CC G4 (IgG4) heavy chain Fc region. This sequence is used to illustrate the
CC method of the invention.

SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 24; Length 327;

Best Local Similarity 100.0%; Pred. No. 2.1e-126;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 61 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 182
DB 121 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 180
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 181 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSKRWQEG 302
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSKRWQEG 300
QY 303 NVFSCSWMEALHNNHYTQKSLSLGK 329
DB 301 NVFSCSWMEALHNNHYTQKSLSLGK 327

RESULT 4

AAE32918
ID AAE32918 standard; Protein; 327 AA.

XX AAE32918;

XX 24-MAR-2003 (first entry)

XX Human immunoglobulin G4 (IgG4) heavy chain Fc region.

XX T-cell; immunogenic; therapy; human; immunoglobulin G4; IgG4.

XX Homo sapiens.

XX WO200279232-A2.

XX 10-OCT-2002.

XX 30-MAR-2002; 2002WO-US09815.

XX 30-MAR-2001; 2001US-280625P.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD;

XX WPI; 2003-103259/09.

XX Reducing the immunogenicity of a fusion protein comprises changing an
PT amino acid within the junction region to reduce the ability of the
PT candidate T-cell epitope identified within the junction spanning to
PT interact with T-cell receptor -
XX Disclosure; Page 53-54; 68pp; English.

XX The invention relates to a method for reducing the immunogenicity of a
CC fusion protein which involves identifying a candidate T-cell epitope
CC within a junction spanning a fusion junction of a fusion protein, and
CC changing an amino acid within the junction region to reduce the ability
CC of the candidate T-cell epitope to interact with a T-cell receptor. The
CC method is useful for reducing the immunogenicity of a fusion protein.
CC It is useful for analysing, changing or modifying one or more amino
CC acids in the junction region of a fusion protein to identify a T-cell
CC epitope and reduce its ability to interact with a T-cell receptor. The
CC less immunogenic fusion proteins are useful in providing therapeutic
CC treatment. The present sequence is human immunoglobulin G4 (IgG4) heavy
CC chain Fc region used to illustrate the method of the invention.

SQ Sequence 327 AA;

Query Match 99.4%; Score 1743; DB 24; Length 327;

Best Local Similarity 100.0%; Pred. No. 2.1e-126;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 61 GLYSLSVVTVFSSSLGTYTCNVNDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 182
DB 121 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 180
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 181 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSKRWQEG 302
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLRTVDSKRWQEG 300

QY 303 NVFSCVMHEALHNHYTKSLSLGK 329
 DB 301 NVFSCVMHEALHNHYTKSLSLGK 327

RESULT 5
 AAW70801
 ID AAW70801 standard; protein; 329 AA.
 XX AAW70801;
 DT 03-FEB-1999 (first entry)
 XX Amino acid sequence of C-gamma-4.
 KW gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 OS Synthetic.
 FH Key
 FT Protein
 FT 2..329
 FT /note= "C-gamma-4"
 PN US8644099-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 27-NOV-1995; 95US-0563105.
 XX
 PR 27-NOV-1995; 95US-0563105.
 PR 20-OCT-1995; 93US-0140222.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Economides A, Stahl N, Yancopoulos GD;
 XX WPI; 1999-044669/04.
 DR
 XX Cytokine antagonists - comprising extracellular domains of
 PT specificity-determining and signal-transducing components of
 PT cytokine receptor
 XX
 PS Example 4; Fig 12; 46pp; English.
 XX
 CC The present sequence represents the amino acid sequence of
 CC C-gamma-4. The protein is used in the course of the invention.
 CC The specification describes cytokine antagonists comprising only the
 CC extracellular domain of the specificity-determining component of
 CC the cytokine receptor and the extracellular domain of a
 CC signal-transducing component of the cytokine receptor. The cytokine
 CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),
 CC granulocyte macrophage colony-stimulating factor (GM-CSF),
 CC gamma-interferon or transforming growth factor-beta (TGF-beta). The
 CC antagonist is capable of binding the cytokine to form a nonfunctional
 CC complex. The compounds have therapeutic activity as cytokine antagonists
 CC and can also be used in assays for identifying novel agonists and
 CC antagonists of cytokines.
 XX
 SQ Sequence 329 AA;
 Query Match 99.4%; Score 1743; DB 20; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.le-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPAPCSRSTSEALGCLVKDYFPPETVSVNSGALTSGVHTRPAVLQSS 62
 DB 3 ASTKGPSVFPAPCSRSTSEALGCLVKDYFPPETVSVNSGALTSGVHTRPAVLQSS 62

QY 63 GLYSLSVVTVPSSSLGTTKTYTCNVNHHKPSNKTVDKRVESKYGPPCPSCPAPEFLGGPSV 122

DB 63 GLYSLSVVTVPSSSLGTTKTYTCNVNHHKPSNKTVDKRVESKYGPPCPSCPAPEFLGGPSV 122
 QY 123 FLFPKPKDITLMIKRTPEVTCVWVDVSOEDPEVQFNWTVDGVVEVHNATKPREEQFNSTY 182
 DB 123 FLFPKPKDITLMIKRTPEVTCVWVDVSOEDPEVQFNWTVDGVVEVHNATKPREEQFNSTY 182
 QY 183 RVVSULTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSOEENTK 242
 DB 183 RVVSULTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSOEENTK 242
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLXSRLLTVDKSRWQEG 302
 DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLXSRLLTVDKSRWQEG 302
 QY 303 NVFSCVMHEALHNHYTKSLSLGK 329
 DB 303 NVFSCVMHEALHNHYTKSLSLGK 329

RESULT 6
 AAY92190
 ID AAY92190 standard; protein; 329 AA.
 XX
 AC AAY92190;
 XX
 DT 01-AUG-2000 (first entry)
 XX
 DE Human IgG1 C-gamma-4 domain.
 XX
 KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;
 KW cytostatic; immunomodulator; osteopathic.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide
 FT 1..2
 FT /note= "ser-Gly bridge"
 FT Protein
 FT 3..329
 FT /label= C-gamma-4
 XX
 PN WO200018932-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 22-SEP-1999; 99WO-US222045.
 XX
 PR 25-SEP-1998; 98US-0101858.
 PR 19-MAY-1999; 99US-0313942.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Stahl N, Yancopoulos GD;
 XX WPI; 2000-293165/25.
 DR
 XX Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 FT
 XX
 PS Example 4; Fig 12; 152pp; English.
 XX
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (sr-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (sr-alpha.beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CNTF (ciliary

neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.

Sequence 329 AA;
Query Match 99.4%; Score 1743; DB 21; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.1e-126;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
Db 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
Db 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
QY 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKATKPREQFNSTY 182
Db 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKATKPREQFNSTY 182
QY 183 RVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242
Db 183 RVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302
Db 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302
QY 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329
Db 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329

RESULT 7
ID AAW13564
AAW13564 standard; Protein; 443 AA.
XX
AC AAW13564;
XX
DT 03-JUN-1997 (first entry)
XX
DE Humanised anti-L-selectin antibody HuDreg 55 heavy chain.

XX L-selectin; humanised antibody; HuDreg 55; acute organ damage;
KW organ failure; poly-trauma; haemorrhagic-traumatic shock.
XX
OS Chimeric Mus sp.;
OS Chimeric Homo sapiens.
XX
PN WC9706822-A1.
XX
XX 27-FEB-1997.
XX
XX 14-AUG-1996; 96WO-US13152.
XX
XX 27-DEC-1995; 95US-0578953.
PR 17-AUG-1995; 95EP-0112895.
PR 19-SEP-1995; 95EP-0114696.
XX
XX (BOE) BOEHRINGER MANNHEIM GMBH.

(PROT-) PROTEIN DESIGN LABS INC.

Co M, Haselbeck A, Martin U, Schumacher G;

WPI; 1997-165036/15.

N-PSDB; AAT61281.

Using anti-selectin antibody to prevent acute organ damage and multiple organ failure - during extracorporeal circulation or following polytrauma, e. g. haemorrhagic-traumatic shock
Disclosure; Page 34-36; 52pp; English.

Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy chains each having the sequence given in AAW13564 and 2 light chains each having the sequence given in AAW13563. These are encoded by the cDNA clones given in AAT61281 and AAT61280. HuDreg 55 can be used to prevent multiple organ failure associated with polytrauma and for the prevention of acute organ damage associated with extracorporeal blood circulation. The antibody inhibits interaction between the carbohydrate-recognising domain of the selectin and the corresponding cell surface receptor.

Sequence 443 AA;

Query Match 99.4%; Score 1743; DB 18; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.1e-126;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
Db 117 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 176
QY 63 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
Db 177 GLYSLSVVTVFSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 236
QY 123 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKATKPREQFNSTY 182
Db 237 FLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKATKPREQFNSTY 296
QY 183 RVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 242
Db 297 RVSVLTVLHQDLNGLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMTK 356
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 302
Db 357 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQEG 416
QY 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329
Db 417 NVFSCSVWHEALHNHYTQKSLSLGLK 443

RESULT 8
AAV31672
ID AAV31672 standard; Protein; 444 AA.
XX
AC AAV31672;
XX
DT 09-NOV-1999 (first entry)
XX
DE Human IgG4 chain C.

XX IgG4; C-gamma-4; antibody; fusion protein; circulating half-life;
KW human; drug delivery.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FT Misc-difference 1.1117 "the identity of these residues is not
FT specified"

XX WO9943713-A1.
 XX PD 02-SEP-1999.
 XX 24-FEB-1999; 99WO-US03966.
 XX PR 25-FEB-1998; 98US-0075887.
 XX PA (LEXI-) LEXIGEN PHARM CORP.
 XX FI Gillies SD, Lan Y, Lo K, Wesolowski J;
 XX DR WPI; 1999-527594/44.
 XX PT New antibody-based fusion proteins, used for the delivery of e.g. a
 XX PT cytokine, ligand-binding protein or protein toxin to target cells in
 XX PT vivo
 XX FS Disclosure; Page 35-36; 41pp; English.
 XX CC The present sequence represents the constant region of human IgG
 XX CC isotype 4 (IgG4, C-gamma-4). C-gamma-1 (see AAY31669) and C-gamma-3
 XX CC (see AAY31671) bind Fc receptors with high affinity whereas C-gamma-4
 XX CC has 10-fold lower binding affinity and C-gamma-2 (see AAY31670) does
 XX CC not bind to Fc receptor gamma-1. The invention provides methods
 XX CC for the genetic construction and expression of antibody-based
 XX CC fusion proteins with enhanced circulating half-lives. The
 XX CC fusion proteins lack the ability to bind to immunoglobulin Fc
 XX CC receptors, either as a consequence of the antibody isotype used
 XX CC for protein construction, i.e. a C-gamma-2 constant region (Fc)
 XX CC or a C-gamma-4 Fc receptor, or through directed mutagenesis of
 XX CC antibody isotypes that normally bind Fc receptors, i.e. C-gamma-1
 XX CC or C-gamma-3. The methods can be used for to increase the
 XX CC circulating half-life of a non-immunoglobulin (Ig) protein such as
 XX CC a cytokine, e.g. tumour necrosis factor (TNF), an interleukin or a
 XX CC lymphokine such as a lymphotoxin or a colony stimulating factor, a
 XX CC ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an
 XX CC interleukin receptor, or a protein toxin (claimed). The fusion
 XX CC proteins are used to deliver selectively the second non-Ig protein
 XX CC to a target cell in vivo so that the second non-Ig protein can
 XX CC exert a localised biological effect.
 XX SQ Sequence 444 AA;
 Query Match 99.4%; Score 1743; DB 20; Length 444;
 Best Local Similarity 100.0%; Pred. No. 3.1e-126; Indels 0; Gaps 0;
 Matches 327; Conservative 0; Mismatches 0;
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 118 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 177
 QY 63 GLYSLSVVTVPPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
 DB 178 GLYSLSVVTVPPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 237
 QY 123 FLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVFNHAKTPREEQFNSTY 182
 DB 238 FLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVFNHAKTPREEQFNSTY 297
 QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPSSQEMTK 242
 DB 298 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPSSQEMTK 357
 QY 243 NOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTTPVLDSDGFFLYSLRTVDKSRWQEG 302
 DB 358 NOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTTPVLDSDGFFLYSLRTVDKSRWQEG 417
 QY 303 NVFCSVNHAEALHNHYTQKSLSLIGK 329
 DB 418 NVFCSVNHAEALHNHYTQKSLSLIGK 444

RESULT 9
 AAW14935
 ID AAW14935 standard; Protein; 463 AA.
 XX AC AAW14935;
 XX DT 16-JUN-1997 (first entry)
 XX DE 2A2 Human IgG4 expression plasmid insert product (heavy chain).
 XX KW Xenotransplantation; graft rejection; cell interaction; pig;
 XX KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 XX KW chimeric antibody; diagnosis.
 XX OS Mus sp.
 XX PN WO9711971-A1.
 XX PD 03-APR-1997.
 XX PF 27-SEP-1996; 96WO-US15575.
 XX PR 26-SEP-1996; 96US-0004489.
 XX PR 28-SEP-1995; 95US-0004489.
 XX PA (ALEX-) ALEXION PHARM INC.
 XX PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 XX PI Rother RP;
 XX DR WPI; 1997-212855/19.
 XX DR N-PSDB; AAT62933.
 XX PT Antibodies binding to porcine but not human cell interaction
 XX PT proteins - useful to treat and assay for rejection of xenografted
 XX PT porcine organs, tissues or cells
 XX PS Disclosure; Page 48-50; 105pp; English.
 XX CC Heavy chain (AAW14935) and light chain (AAW14936) sequences
 XX CC correspond to murine anti-porcine soluble vascular cell adhesion
 XX CC molecule (VCAM) monoclonal antibody 2A2 (see also AAW14931-32). They
 XX CC are encoded by a 2A2 human IgG4 expression plasmid insert (see
 XX CC also AAT62933). A chimeric antibody specific for porcine VCAM can be
 XX CC produced in transfected host cells. It is useful for diagnosing
 XX CC human rejection of porcine xenotransplants and for improving
 XX CC xenotransplantation of porcine cells, tissues and organs into human
 XX CC recipients.
 XX SQ Sequence 463 AA;
 Query Match 99.4%; Score 1743; DB 18; Length 463;
 Best Local Similarity 100.0%; Pred. No. 3.2e-126; Indels 0; Gaps 0;
 Matches 327; Conservative 0; Mismatches 0;
 QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 62
 DB 137 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 196
 QY 63 GLYSLSVVTVPPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
 DB 197 GLYSLSVVTVPPSSSLGKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 256
 QY 123 FLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVFNHAKTPREEQFNSTY 182
 DB 257 FLFPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVFNHAKTPREEQFNSTY 316
 QY 183 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPSSQEMTK 242
 DB 317 RVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYITLPSSQEMTK 376
 QY 243 NOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTTTPVLDSDGFFLYSLRTVDKSRWQEG 302

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Db 377 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSLRLTVDKSRWQEG 436
QY 303 NVFSCSVMEALHNHYTKSLSLGK 329
Db 437 NVFSCSVMEALHNHYTKSLSLGK 463

RESULT 10
AAW14932
ID AAW14932 standard; Protein; 463 AA.
XX
AC AAW14932;
XX
DT 16-JUN-1997 (first entry)
XX
DE Murine anti-porcine VCAM 2A2 heavy chain.
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 50..54
FT /label= CDR1
FT Region 69..85
FT /label= CDR2
FT Region 118..125
FT /label= CDR3
XX
PN WO9711971-A1.
XX
PD 03-APR-1997.
XX
PF 27-SEP-1996; 96WO-US15575.
XX
PR 26-SEP-1996; 96US-0004489.
XX
PR 28-SEP-1995; 95US-0004489.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI Rother RP;
XX
DR WPI: 1997-212855/19.
DR N-PSDB; AAT62930.
XX
PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells
XX
PS Disclosure; Page 40-42; 105pp; English.
XX
CC Heavy chain (AAW14932) and light chain (AAW14931) sequences are
CC provided for the murine anti-porcine soluble vascular cell adhesion
CC molecule (VCAM) monoclonal antibody (Mab) 2A2. Hybridoma 2A2 was
CC produced by standard techniques using recombinant, soluble porcine
CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
CC Mab 2A2 and 3F4 (see also AAW14937-38) variable regions into
CC expression plasmid pAPEX-3P modified to contain the human gamma4
CC constant region in place of the human gamma1 CI region. Sequences
CC are provided for 2A2 (chimeric) human G2/G4 cDNA (AAW14933), a 2A2
CC human G2/G4 expression plasmid insert product (AAW14934), and 2A2
CC human IG4 expression plasmid insert products (AAW14935-36). The
CC chimeric antibodies are specific for porcine VCAM. They are useful
CC for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs
CC into human recipients.
XX
SQ Sequence 463 AA;

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Query Match 99.4%; Score 1743; DB 18; Length 463;
Best Local Similarity 100.0%; Pred. No. 3.2e-126;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 137 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 196
QY 63 GLYSLSSVTVFSSSLGTITTCNVDPKPSNTKVDKRVEKYGPCCPAPEFLGQPSV 122
Db 197 GLYSLSSVTVFSSSLGTITTCNVDPKPSNTKVDKRVEKYGPCCPAPEFLGQPSV 256
QY 123 FLPPPKKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
Db 257 FLPPPKKDTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 316
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYVTLPPSQEEMTK 242
Db 317 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYVTLPPSQEEMTK 376
QY 243 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSLRLTVDKSRWQEG 302
Db 377 NQVSLTCLVKGYPSPDIWVESNGQPNENYKTTPEVLDSGSPFLYSLRLTVDKSRWQEG 436
QY 303 NVFSCSVMEALHNHYTKSLSLGK 329
Db 437 NVFSCSVMEALHNHYTKSLSLGK 463

RESULT 11
AAW14941
ID AAW14941 standard; Protein; 464 AA.
XX
AC AAW14941;
XX
DT 16-JUN-1997 (first entry)
XX
DE 3F4 Human IgG4 expression plasmid insert product (heavy chain).
XX
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Mus sp.
XX
PN WO9711971-A1.
XX
PD 03-APR-1997.
XX
PF 27-SEP-1996; 96WO-US15575.
XX
PR 26-SEP-1996; 96US-0004489.
XX
PR 28-SEP-1995; 95US-0004489.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
PI Rother RP;
XX
DR WPI: 1997-212855/19.
DR N-PSDB; AAT62938.
XX
PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells
XX
PS Disclosure; Page 62-64; 105pp; English.
XX
CC Heavy chain (AAW14941) and light chain (AAW14942) sequences
CC correspond to murine anti-porcine soluble vascular cell adhesion
CC molecule (VCAM) monoclonal antibody 3F4 (see also AAW14937-38). They
CC are encoded by a 3F4 human IgG4 expression plasmid insert (see
CC also AAT62938). A chimeric antibody specific for porcine VCAM can be

```

CC produced in transfected host cells. It is useful for diagnosing
 CC human rejection of porcine xenotransplants and for improving
 CC xenotransplantation of porcine cells, tissues and organs into human
 CC recipients.
 XX Sequence 464 AA;
 SQ

Query Match 99.4%; Score 1743; DB 18; Length 464;
 Best Local Similarity 100.0%; Pred. No. 3.2e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 138 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
 QY 63 GLYSLSSVTVTPSSSLGKTTCNVDRKPSNTKYDKRVESKYGPPCPSCPAPEFLGGPSV 122
 DB 198 GLYSLSSVTVTPSSSLGKTTCNVDRKPSNTKYDKRVESKYGPPCPSCPAPEFLGGPSV 257
 QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 182
 DB 258 FLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 317
 QY 183 RVSVSLTVLHQDLWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
 DB 318 RVSVSLTVLHQDLWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 377
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLRTVDSRWQEG 302
 DB 378 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLRTVDSRWQEG 437
 QY 303 NVFSCSVMHAEALHNHYTQKSLSLGLK 329
 DB 438 NVFSCSVMHAEALHNHYTQKSLSLGLK 464

RESULT 12
 AAW14938
 ID AAW14938 standard; Protein; 464 AA.
 XX AAW14938;
 XX
 DT 16-JUN-1997 (first entry)
 XX
 DE Murine anti-porcine VCAM 3F4 heavy chain.
 XX
 KW Xenotransplantation; graft rejection; cell interaction; pig;
 KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
 KW chimeric antibody; diagnosis.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 50..54
 FT /label= CDR1
 FT Region 69..85
 FT /label= CDR2
 FT Region 118..126
 FT /label= CDR3
 XX
 PN WO9711971-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 27-SEP-1996; 96WO-US15575.
 XX
 PR 26-SEP-1996; 96US-0004489.
 PR 28-SEP-1995; 95US-0004489.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matis LA, Mueller EE, Mueller JP, Rollins S;
 PI Rother RP;

XX WPI; 1997-212855/19.
 DR N-PSDB; AAT62935.
 XX
 PT Antibodies binding to porcine but not human cell interaction
 PT proteins - useful to treat and assay for rejection of xenografted
 PT porcine organs, tissues or cells
 XX
 PS Disclosure; Page 53-55; 105pp; English.
 XX
 CC Heavy chain (AAW14938) and light chain (AAW14937) sequences are
 CC provided for the murine anti-porcine soluble vascular cell adhesion
 CC molecule (VCAM) monoclonal antibody (MAB) 3F4. Hybridoma 3F4 was
 CC produced by standard techniques using recombinant, soluble porcine
 CC VCAM as immunogen. Chimeric antibodies can be produced by cloning
 CC MAB 3F4 and 2A2 (see also AAW14931-32) variable regions into
 CC expression plasmid PAPEX-3P modified to contain the human gamma4
 CC constant region in place of the human gamma1 C1 region. Sequences
 CC are provided for 3F4 (chimeric) human G2/G4 cDNA (AAW14939), a 3F4
 CC human G2/G4 expression plasmid insert products (AAW14940), and 3F4
 CC human IgG4 expression plasmid insert products (AAW14941-42). The
 CC chimeric antibodies are specific for porcine VCAM. They are useful
 CC for diagnosing human rejection of porcine xenotransplants and for
 CC improving xenotransplantation of porcine cells, tissues and organs
 CC into human recipients.
 XX
 CC Sequence 464 AA;
 SQ

Query Match 99.4%; Score 1743; DB 18; Length 464;
 Best Local Similarity 100.0%; Pred. No. 3.2e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 138 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
 QY 63 GLYSLSSVTVTPSSSLGKTTCNVDRKPSNTKYDKRVESKYGPPCPSCPAPEFLGGPSV 122
 DB 198 GLYSLSSVTVTPSSSLGKTTCNVDRKPSNTKYDKRVESKYGPPCPSCPAPEFLGGPSV 257
 QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 182
 DB 258 FLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTPREEQFNSTY 317
 QY 183 RVSVSLTVLHQDLWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
 DB 318 RVSVSLTVLHQDLWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 377
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLRTVDSRWQEG 302
 DB 378 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFPLYSLRTVDSRWQEG 437
 QY 303 NVFSCSVMHAEALHNHYTQKSLSLGLK 329
 DB 438 NVFSCSVMHAEALHNHYTQKSLSLGLK 464

RESULT 13
 AAR80617
 ID AAR80617 standard; Protein; 467 AA.
 XX AAR80617;
 AC
 XX
 DT 19-APR-1996 (first entry)
 XX
 DE Anti-human IL-4 humanised MAB h25D2-9 mature heavy chain.
 XX
 KW Anti-human interleukin-4; IL-4; humanised; purification;
 KW treatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9;
 KW antibody.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Peptide /label= leader_sequence
 FT Peptide 20..467
 FT Peptide /label= mat_peptide
 XX WO9524481-A2.
 PN
 XX
 XX 14-SEP-1995.
 XX 08-MAR-1995; 95WO-US02400.
 XX 10-MAR-1994; 94US-0208886.
 PR
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX
 XX Dalie B, Miller K, Murgolo N, Tindall S;
 PI
 XX WPI; 1995-328272/42.
 DR
 XX
 XX Humanised monoclonal antibody against human interleukin (IL)-4 -
 PT has increased binding affinity and expression, and hence greater
 PT therapeutic value in the treatment of IL-4 related diseases
 PT
 XX
 XX Claim 3; Pages 109-110; 116pp; English.
 PS
 XX
 XX AAR80617 is the anti-human IL-4 humanised monoclonal antibody (MAB)
 CC h25D2-9, mature heavy chain. It can be used for the prepn.,
 CC purificn. and immunoassay of the humanised Abs. Pharmaceutical
 CC compns. and anti-idiotypic Abs (against the MAB) can also be
 CC prepd. for the treatment of IL-4 related diseases by respectively
 CC suppressing, or initiating the binding activity of IL-4. The
 CC humanised MAB is derived from the rodent. MAB 25D2.
 CC
 XX
 SQ Sequence 467 AA;
 Query Match 99.4%; Score 1743; DB 16; Length 467;
 Best Local Similarity 100.0%; Pred. No. 3.3e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 62
 DB 141 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 200
 QY 63 GLYSLSVTVTPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFLGGPSV 122
 DB 201 GLYSLSVTVTPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFLGGPSV 260
 QY 123 FLPPPKPKDTLMISRTPEVTCVVVDVSDPEQDFVFNWYDGVGVHNAAKTPKEEQFNSTY 182
 DB 261 FLPPPKPKDTLMISRTPEVTCVVVDVSDPEQDFVFNWYDGVGVHNAAKTPKEEQFNSTY 320
 QY 183 RVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSSEEMTK 242
 DB 321 RVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSSEEMTK 380
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
 DB 381 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 440
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
 DB 441 NVFSCSVMEALHNHYTQKSLSLGLK 467
 RESULT 14
 ID AAW14925
 XX AAW14925 standard; Protein; 467 AA.
 AC AAW14925;
 XX
 XX 18-OCT-1997 (first entry)
 DT
 XX

DE Human gamma-4 heavy chain.
 XX
 XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma 4.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO9709351-A1.
 PN
 XX 13-MAR-1997.
 PD
 XX 05-SEP-1996; 96WO-US14324.
 PF
 XX 06-SEP-1995; 95US-0523894.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 PA
 XX
 XX Hanna N, Newman RA, Reff ME;
 PI
 XX WPI; 1997-201913/18.
 DR
 XX N-PSDB; AAT62868.
 DR
 XX
 XX Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 PT
 XX
 XX Claim 6; Page 82-84; 155pp; English.
 PS
 XX
 XX 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
 CC regions of human gamma-4, gamma-4E carrying an L236E mutation in
 CC the hinge region, and gamma-4PE carrying L236S and S229P mutations.
 CC They can be incorporated into novel monoclonal and chimeric
 CC antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in
 CC which the human IgG4 Fc binding domain framework is combined with
 CC the antigen binding domains (see also AAW14922-23) of macaque anti-
 CC human CD4 monoclonal antibody B9.1. These antibodies show high
 CC affinity to human CD4, have little or no immunogenicity in humans
 CC and show reduced or absence of effector function. They can be used
 CC to treat autoimmune diseases such as rheumatoid arthritis.
 CC
 XX
 SQ Sequence 467 AA;
 Query Match 99.4%; Score 1743; DB 16; Length 467;
 Best Local Similarity 100.0%; Pred. No. 3.3e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 62
 DB 141 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVMSWNSGALTSGVHTFPAVLQSS 200
 QY 63 GLYSLSVTVTPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFLGGPSV 122
 DB 201 GLYSLSVTVTPSSSLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFLGGPSV 260
 QY 123 FLPPPKPKDTLMISRTPEVTCVVVDVSDPEQDFVFNWYDGVGVHNAAKTPKEEQFNSTY 182
 DB 261 FLPPPKPKDTLMISRTPEVTCVVVDVSDPEQDFVFNWYDGVGVHNAAKTPKEEQFNSTY 320
 QY 183 RVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSSEEMTK 242
 DB 321 RVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSSEEMTK 380
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
 DB 381 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 440
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
 DB 441 NVFSCSVMEALHNHYTQKSLSLGLK 467

RESULT 15
 AAR28808
 ID AAR28808 standard; Protein; 468 AA.
 XX AC AAR28808;
 XX AC AAR28808;
 DT 25-MAR-2003 (updated)
 DT 02-APR-1993 (first entry)
 XX DE pre-5A8 humanised heavy chain.
 XX KW Vector; pMDR1002; NotI; HindIII; pMDR1001; pSAB132; pBAG101; E. coli;
 KW JA221(Ig); ampicillin; resistance; immunoglobulin; signal sequence;
 KW humanised; 5A8; heavy chain; variable; region; HV; IGH4; constant;
 KW HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
 KW lymphocytes; helper; inducer; HIV; syncytia; formation.
 XX KW Synthetic.
 XX OS
 XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Immunoglobulin signal peptide"
 FT Region 20..141
 FT /note= "Humanised 5A8 HV"
 FT Region 142..468
 FT /note= "Human IGH4 HC"
 XX PN WO9209305-A1.
 XX PD 11-JUN-1992.
 XX PF 27-NOV-1991; 91WO-US08843.
 XX PR 27-NOV-1990; 90US-0618542.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
 XX WPI; 1992-398399/48.
 XX DR N-PSDB; AAQ30910.
 XX PT New anti-CD4 antibody homologues - which bind CD4, do not block
 PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
 PT formation between CD4+ cells
 XX PS Disclosure; Page 155-56; 205pp; English.
 XX CC This sequence is encoded by the insert of the vector pMDR1002. Three
 CC fragments were used in the construction of pMDR1002; a 443 bp NotI/
 CC HindIII fragment of pMDR1001 (see AAQ30905), the 7913 bp NotI linearised
 CC PSAB132 (see AAQ30906) and a 2109 bp NotI/HindIII fragment of pBAG101
 CC (see AAQ30909). These fragments were ligated together and the ligation
 CC mixture was used to transform E. coli JA221(Ig) to ampicillin
 CC resistance. This sequence represents the immunoglobulin signal
 CC sequence, amino acids (AA) 1-122 of the humanised 5A8 heavy chain
 CC variable region (HV) and AA114-AA478 of the human IGH4 heavy chain,
 CC ie. the constant region (HC). This polypeptide is an antibody homolog
 CC which was shown to bind to CD4 but did not block the binding of gp120
 CC to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes
 CC (helper/inducer cells). The homolog blocked HIV-induced syncytia
 CC formation. This homolog can be used in the detection, prophylaxis
 CC and treatment of diseases caused by infective agents whose primary
 CC targets are CD4+ cells.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 468 AA;

Query Match 99.4%; Score 1743; DB 13; Length 468;
 Best Local Similarity 100.0%; Pred. No. 3.3e-126;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
 DB 142 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 201
 QY 63 GLYSLSVVTVFPSSSLGKTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
 DB 202 GLYSLSVVTVFPSSSLGKTTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 261
 QY 123 FLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 182
 DB 262 FLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 321
 QY 183 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISAKQOPREPOQYVITLPPSQEEMTK 242
 DB 322 RVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISAKQOPREPOQYVITLPPSQEEMTK 381
 QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
 DB 382 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 441
 QY 303 NVFSCSVWHEALHNHYTOKSLSLGK 329
 DB 442 NVFSCSVWHEALHNHYTOKSLSLGK 468

Search completed: January 13, 2004, 12:38:29
 Job time : 78.7188 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 52.5825 Seconds
(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-100

Perfect score: 1754
Sequence: 1 EFASKGPSVFPPLAPCSRST.....MHEALHNHYTKSLSLGK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747907 segs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1754	100.0	329	11	US-09-990-586-100
2	1754	100.0	329	12	US-10-310-113-169
3	1754	100.0	329	12	US-10-230-880-100
4	1743	99.4	327	12	US-09-925-664-47
5	1743	99.4	327	12	US-10-112-582-4
6	1743	99.4	327	12	US-10-310-719-7
7	1743	99.4	327	14	US-10-047-542-26
8	1743	99.4	329	10	US-09-935-868-12
9	1743	99.4	329	12	US-10-282-162-12
10	1743	99.4	329	15	US-10-287-035-12
11	1743	99.4	443	9	US-09-917-410-4
12	1743	99.4	444	11	US-09-256-156-4
13	1743	99.4	448	9	US-09-917-410-6
14	1743	99.4	465	12	US-10-401-344-2
15	1743	99.4	467	15	US-10-211-357-8

16	1738	99.1	467	12	US-10-428-408A-30	Sequence 30, Appl
17	1736	99.0	467	15	US-10-211-357-10	Sequence 10, Appl
18	1731	98.7	467	15	US-10-211-357-12	Sequence 12, Appl
19	1649.5	94.0	472	12	US-10-307-724-67	Sequence 67, Appl
20	1649.5	94.0	472	15	US-10-006-593-67	Sequence 57, Appl
21	1638.5	93.4	580	12	US-10-310-719-37	Sequence 37, Appl
22	1611.5	91.9	530	8	US-08-485-163-5	Sequence 4, Appl
23	1611.5	91.9	530	9	US-09-766-995-4	Sequence 4, Appl
24	1605.5	91.5	326	12	US-10-112-582-2	Sequence 2, Appl
25	1605.5	91.5	326	12	US-10-310-719-9	Sequence 9, Appl
26	1605.5	91.5	326	14	US-10-047-542-22	Sequence 22, Appl
27	1605.5	91.5	433	11	US-09-256-156-2	Sequence 2, Appl
28	1605.5	91.5	433	15	US-10-153-382-17	Sequence 17, Appl
29	1605.5	91.5	463	15	US-10-153-382-3	Sequence 3, Appl
30	1605.5	91.5	463	15	US-10-153-382-13	Sequence 13, Appl
31	1605.5	91.5	464	15	US-10-153-382-9	Sequence 9, Appl
32	1605.5	91.5	470	10	US-09-859-053-28	Sequence 28, Appl
33	1605.5	91.5	470	10	US-09-859-053-32	Sequence 32, Appl
34	1605.5	91.5	470	10	US-09-859-053-35	Sequence 35, Appl
35	1604.5	91.5	468	15	US-10-071-485-67	Sequence 67, Appl
36	1604.5	91.5	711	15	US-10-071-485-90	Sequence 90, Appl
37	1601.5	91.3	332	11	US-09-990-586-98	Sequence 98, Appl
38	1601.5	91.3	332	12	US-10-310-113-167	Sequence 167, Appl
39	1601.5	91.3	332	12	US-10-230-880-98	Sequence 98, Appl
40	1599.5	91.2	330	12	US-10-366-709-52	Sequence 52, Appl
41	1599.5	91.2	450	9	US-09-796-848A-37	Sequence 37, Appl
42	1599.5	91.2	450	9	US-09-796-848A-39	Sequence 39, Appl
43	1599.5	91.2	450	9	US-09-796-848A-41	Sequence 41, Appl
44	1599.5	91.2	450	9	US-09-796-848A-43	Sequence 43, Appl
45	1599.5	91.2	450	9	US-09-796-848A-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-990-586-100
; Sequence 100, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-100

Query Match	100.0%;	Score 1754;	DB 11;	Length 329;
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Matches 329,	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EFASKGPSVFPPLAPCSRSTSESTAALGCLVKDIFPEPTVSNVNSGALTSGVHTFPAVLQ	60	
Db	1	EFASKGPSVFPPLAPCSRSTSESTAALGCLVKDIFPEPTVSNVNSGALTSGVHTFPAVLQ	60	
Qy	61	SSGLYSLSSVVTVFPPSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCSCPAPFLGGP	120	
Db	61	SSGLYSLSSVVTVFPPSSSLGKTKYTCNVDRKPSNTKVDKRVESKYGPPCSCPAPFLGGP	120	
Qy	121	SVFLFPPKPKDITLMISRTPEVTCVVDVDSQEDDEVDQFNWTVDGVVHNATKTRERQFNS	180	
Db	121	SVFLFPPKPKDITLMISRTPEVTCVVDVDSQEDDEVDQFNWTVDGVVHNATKTRERQFNS	180	

QY 181 TYRVSVLTCLVKGFPSPDIKAVESNGQPPENNYKTPPVLDSGDSFFLYSLRTVDKSRWQ 240
Db 181 TYRVSVLTCLVKGFPSPDIKAVESNGQPPENNYKTPPVLDSGDSFFLYSLRTVDKSRWQ 240
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Db 241 TKQVSLTCLVKGFPSPDIKAVESNGQPPENNYKTPPVLDSGDSFFLYSLRTVDKSRWQ 300
QY 301 EGNVFCSCVMHEALHNYTKQSLSLGK 329
Db 301 EGNVFCSCVMHEALHNYTKQSLSLGK 329

RESULT 2

US-10-310-113-169
; Sequence 169, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAC, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71759)
; CURRENT APPLICATION NUMBER: US/10/310,113
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/914,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 169
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-169

Query Match 100.0%; Score 1754; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.7e-140;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EFASITKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
Db 1 EFASITKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 60
QY 61 SSGLYSLSSVTVFPSSSLGKTYTCNVDPKNTKVDKRVESKYGPPCPAPAEFLGGP 120
Db 61 SSGLYSLSSVTVFPSSSLGKTYTCNVDPKNTKVDKRVESKYGPPCPAPAEFLGGP 120
QY 121 SVFLFPPKPKDTLMISRTPEVTCVVDVSEQDEPEVQFNWYDGVVHNATKPREEQFNS 180
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Db 301 EGNVFCSCVMHEALHNYTKQSLSLGK 329

RESULT 3

US-10-310-113-169

US-10-230-880-100
; Sequence 100, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 100
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-100

Query Match 100.0%; Score 1754; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.7e-140;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 SSGLYSLSSVTVFPSSSLGKTYTCNVDPKNTKVDKRVESKYGPPCPAPAEFLGGP 120
Db 61 SSGLYSLSSVTVFPSSSLGKTYTCNVDPKNTKVDKRVESKYGPPCPAPAEFLGGP 120
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RESULT 4

US-09-925-664-47
; Sequence 47, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
; APPLICANT: Denney, Jr., Dan W.
; TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
; FILE REFERENCE: GENITOP-08499
; CURRENT APPLICATION NUMBER: US/09/925,664
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/370,453
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: 08/644,664
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/761,277
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 47

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; LENGTH: 327
; TYPE: PRT
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US-09-925-664-47

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QY 183 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 242
Db 181 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 240

QY 243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300

QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 5
US-10-112-582-4
; Sequence 4, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Ig gamma-4 chain C region
US-10-112-582-4

Query Match
Best Local Similarity 99.4%; Score 1743; DB 12; Length 327;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVTVTPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 122
Db 61 GLYSLSVTVTPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 120

QY 123 FLPPPKPOTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
Db 121 FLPPPKPOTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 180
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QY 183 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 242
Db 181 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 240

QY 243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300

QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 6
US-10-310-719-7
; Sequence 7, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc
; LOCATION: (1)..(327)
; OTHER INFORMATION: Human gamma 4 constant region
US-10-310-719-7

Query Match
Best Local Similarity 99.4%; Score 1743; DB 12; Length 327;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSVTVTPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 122
Db 61 GLYSLSVTVTPSSSLGTTKTYTCNVDPKSNKVDKRVESKYGPPCPAPFELGGPSV 120

QY 123 FLPPPKPOTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
Db 121 FLPPPKPOTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNATKPREEQFNSTY 180

QY 183 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 242
Db 181 RVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPPSQEEMTK 240

QY 243 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 300

QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGLK 327

RESULT 7
US-10-047-542-26
; Sequence 26, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
```



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; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.C1P1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-26

Query Match          99.4%; Score 1743; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
DB 121 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 180
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 181 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 300
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
DB 301 NVFSCSVMEALHNNHYTKQSLSLGK 327

RESULT 8
US-09-935-868-12
; Sequence 12, Application US/09935868
; Patent No. US2002016490A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-12

Query Match          99.4%; Score 1743; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
DB 121 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 180
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 181 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 300
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
DB 301 NVFSCSVMEALHNNHYTKQSLSLGK 327

Query Match          99.4%; Score 1743; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 1 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 61 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
DB 121 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 180
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 181 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
DB 241 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 300
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
DB 301 NVFSCSVMEALHNNHYTKQSLSLGK 327
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DB 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
DB 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
DB 303 NVFSCSVMEALHNNHYTKQSLSLGK 329

RESULT 9
US-10-282-162-12
; Sequence 12, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-12

Query Match          99.4%; Score 1743; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
DB 3 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 62
QY 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 63 GLYSLSSVTVTPSSSLGKTYTCNVDRKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
QY 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
DB 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY 182
QY 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
DB 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
DB 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLRTVDKSRWQEG 302
QY 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
DB 303 NVFSCSVMEALHNNHYTKQSLSLGK 329
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Db 303 NVFSCVMHEALHNHYTQKSLSLGK 329

RESULT 10

US-10-287-035-12

Sequence 12, Application US/10287035

Publication No. US20030104567A1

GENERAL INFORMATION:

APPLICANT: Neil Stahl and George D. Yancopoulos

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203DA

CURRENT APPLICATION NUMBER: US/10/287,035

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: USSN 09/935,868

PRIOR FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: USSN 09/787,835

PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: USSN 09/313,942

PRIOR FILING DATE: 1998-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 12

LENGTH: 329

TYPE: PRT

ORGANISM: Homo sapiens

US-10-287-035-12

Query Match 99.4%; Score 1743; DB 15; Length 329;

Best Local Similarity 100.0%; Pred. No. 1.4e-139;

Mismatches 0; Indels 0; Gaps 0;

Matches 327; Conservative 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

Db 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

QY 63 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 122

Db 63 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 122

QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRREQFNSTY 182

Db 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRREQFNSTY 182

QY 183 RVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

Db 183 RVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

QY 243 NVQSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 243 NVQSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

QY 303 NVFSCVMHEALHNHYTQKSLSLGK 329

Db 303 NVFSCVMHEALHNHYTQKSLSLGK 329

RESULT 11

US-09-917-410-4

Sequence 4, Application US/09917410

Patent No. US20020098183A1

GENERAL INFORMATION:

APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;

CO, Man S.

TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF

MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR

PREVENTION OF ACUTE ORGAN DAMAGE AFTER

EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII, WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/917,410

FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: <Unknown>

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. US20020098183A1man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-917-410-4

Query Match 99.4%; Score 1743; DB 9; Length 443;

Best Local Similarity 100.0%; Pred. No. 2.1e-139;

Mismatches 0; Indels 0; Gaps 0;

Matches 327; Conservative 0;

QY 3 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 62

Db 117 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNLSGALTSGVHTFPAVLQSS 176

QY 63 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 122

Db 177 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSV 236

QY 123 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRREQFNSTY 182

Db 237 FLFPPKPKDTLMISRTPEVTCVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPRREQFNSTY 296

QY 183 RVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242

Db 297 RVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 356

QY 243 NVQSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302

Db 357 NVQSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 416

QY 303 NVFSCVMHEALHNHYTQKSLSLGK 329

Db 417 NVFSCVMHEALHNHYTQKSLSLGK 443

RESULT 12

US-09-256-156-4

Sequence 4, Application US/09256156A

Publication No. US20030105294A1

GENERAL INFORMATION:

APPLICANT: GILLIES, Stephen D

APPLICANT: LO, Kin-Ming
APPLICANT: LAN, Yan
APPLICANT: WESOLOWSKI, John
TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
FILE REFERENCE: LEX-003
CURRENT APPLICATION NUMBER: US/09/256,156A
CURRENT FILING DATE: 1999-02-24
EARLIER APPLICATION NUMBER: US 60/075,887
EARLIER FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 4
LENGTH: 444
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: IGG-4 CHAIN C REGION
NAME/KEY: VARIANT
LOCATION: (1)..(117)
OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved
OTHER INFORMATION: amino acids
US-09-256-156-4

Query Match 99.4%; Score 1743; DB 11; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.1e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
DB 118 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 177

QY 63 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 178 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 237

QY 123 FLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
DB 238 FLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 297

QY 183 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242
DB 298 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 357

QY 243 NOVSLTCLVKGYPSPDI AVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQEG 302
DB 358 NOVSLTCLVKGYPSPDI AVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQEG 417

QY 303 NVFSCVMHEALHNHYTKLSLSLKG 329
DB 418 NVFSCVMHEALHNHYTKLSLSLKG 444

RESULT 13
US-09-917-410-6
Sequence 6, Application US/09917410
Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO. Man S.
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION DATA: US/09/917,410
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 13-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-917-410-6

Query Match 99.4%; Score 1743; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.2e-139; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
DB 122 ASTKPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 181

QY 63 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
DB 182 GLYSLSVVTPSSSLGKTKYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 241

QY 123 FLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 182
DB 242 FLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 301

QY 183 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 242
DB 302 RVVSVLTVLHQDLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTK 361

QY 243 NOVSLTCLVKGYPSPDI AVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQEG 302
DB 362 NOVSLTCLVKGYPSPDI AVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKSRWQEG 421

QY 303 NVFSCVMHEALHNHYTKLSLSLKG 329
DB 422 NVFSCVMHEALHNHYTKLSLSLKG 448

RESULT 14
US-10-401-344-2
Sequence 2, Application US/10401344
Publication No. US20030194404A1
GENERAL INFORMATION:
APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Greenfeder, Scott
APPLICANT: Corvalan, Jose
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COM
TITLE OF INVENTION: COMPRISING SAME
FILE REFERENCE: L101564W1
CURRENT APPLICATION NUMBER: US/10/401,344
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patent in version 3.1

SEQ ID NO 2
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1) (19)
OTHER INFORMATION:
FEATURE:
NAME/KEY: Variable Region
LOCATION: (20) (138)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH1 Region
LOCATION: (139) (236)
OTHER INFORMATION:
FEATURE:
NAME/KEY: Hinge Region
LOCATION: (237) (248)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH2 Region
LOCATION: (249) (358)
OTHER INFORMATION:
FEATURE:
NAME/KEY: CH3 Region
LOCATION: (359) (465)
OTHER INFORMATION:
US-10-401-344-2

Query Match 99.4%; Score 1743; DB 12; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.3e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGSVPFLAPCSRSTSESTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 139 ASTKGSVPFLAPCSRSTSESTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 198
Qy 63 GLYSLSSVTVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 122
Db 199 GLYSLSSVTVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 258
Qy 123 FLPPPKPDLMISRTPETVTCVVDVSQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 182
Db 259 FLPPPKPDLMISRTPETVTCVVDVSQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 318
Qy 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
Db 319 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 378
Qy 243 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 379 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 438
Qy 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329
Db 439 NVFSCSVWHEALHNHYTQKSLSLGLK 465

RESULT 15
US-10-211-357-8
Sequence 8, Application US/10211357
Publication No. US2003007275A1
GENERAL INFORMATION:

APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street

CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211.357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612.914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523.894
FILING DATE: 06-SEP-1995

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-211-357-8

Query Match 99.4%; Score 1743; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.3e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 ASTKGSVPFLAPCSRSTSESTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGSVPFLAPCSRSTSESTAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSSVTVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 122
Db 201 GLYSLSSVTVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAEPFLGGPSV 260
Qy 123 FLPPPKPDLMISRTPETVTCVVDVSQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 182
Db 261 FLPPPKPDLMISRTPETVTCVVDVSQEDPEVQFNWYDGVGVHNAKTKPREEQFNSTY 320
Qy 183 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 242
Db 321 RVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK 380
Qy 243 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 381 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEG 440
Qy 303 NVFSCSVWHEALHNHYTQKSLSLGLK 329
Db 441 NVFSCSVWHEALHNHYTQKSLSLGLK 467

Search completed: January 13, 2004, 13:13:47
Job time : 53.5825 secs

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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 28.4463 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-100
Perfect score: 1754
Sequence: 1 EFASKGSPVFLAPCSRST.....MHEALHNYTKSLSLSGK 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/aaa/5A.COMB.pdp.*
2: /cgn2_6/ptodata/1/aaa/5B.COMB.pdp.*
3: /cgn2_6/ptodata/1/aaa/6A.COMB.pdp.*
4: /cgn2_6/ptodata/1/aaa/6B.COMB.pdp.*
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6: /cgn2_6/ptodata/1/aaa/Backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	99.4	327	2	US-08-761-277A-47
2	1743	99.4	329	4	US-09-313-942-12
3	1743	99.4	443	5	PCT-US96-13152-4
4	1743	99.4	467	1	US-08-704-744-81
5	1743	99.4	467	3	US-08-523-894-8
6	1736	99.0	467	3	US-08-523-894-10
7	1731	98.7	467	3	US-08-523-894-12
8	1726.5	98.4	467	2	US-07-916-098A-45
9	1611.5	91.9	530	3	US-08-477-460B-4
10	1611.5	91.9	530	3	US-08-379-516-4
11	1611.5	91.9	530	3	US-09-329-916-4
12	1611.5	91.9	530	3	US-08-485-372A-4
13	1611.5	91.9	530	4	US-09-409-006A-4
14	1611.5	91.9	530	4	US-08-484-681-4
15	1611.5	91.9	530	5	PCT-US93-07422-4
16	1604.5	91.5	468	4	US-09-485-737B-67
17	1604.5	91.5	711	4	US-09-485-737B-90
18	1599.5	91.2	473	3	US-09-049-672A-4
19	1596.5	91.0	330	4	US-09-301-593-22
20	1596.5	91.0	451	2	US-08-887-352B-14
21	1596.5	91.0	451	2	US-08-887-352B-16
22	1596.5	91.0	451	2	US-08-887-352B-18
23	1596.5	91.0	451	3	US-08-466-151-65
24	1596.5	91.0	451	3	US-09-109-207C-14
25	1596.5	91.0	451	3	US-09-109-207C-16
26	1596.5	91.0	451	3	US-09-109-207C-18
27	1596.5	91.0	451	3	US-09-282-505-2

28	1596.5	91.0	451	3	US-09-054-255-2
29	1596.5	91.0	451	3	US-09-296-005-14
30	1596.5	91.0	451	3	US-09-296-005-16
31	1596.5	91.0	451	3	US-09-296-005-18
32	1596.5	91.0	451	4	US-09-282-846-2
33	1596.5	91.0	451	4	US-09-680-145-2
34	1596.5	91.0	452	3	US-09-027-449-71
35	1596.5	91.0	452	3	US-09-026-985-71
36	1596.5	91.0	452	4	US-09-121-952A-71
37	1596.5	91.0	452	4	US-09-234-340A-71
38	1596.5	91.0	453	4	US-09-301-593-18
39	1596.5	91.0	454	2	US-07-934-373C-22
40	1596.5	91.0	454	3	US-08-437-643B-22
41	1596.5	91.0	454	4	US-08-146-206C-22
42	1596.5	91.0	454	5	PCT-US93-07832-22
43	1596.5	91.0	467	3	US-09-049-672A-8
44	1594.5	90.9	450	2	US-08-788-800-12
45	1594.5	90.9	469	2	US-07-934-373C-23

ALIGNMENTS

RESULT 1
US-08-761-277A-47
; Sequence 47, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENITOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-761-277A-47

Query Match 99.4%; Score 1743; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 7.8e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 ASTKGSVPFLAPCSRSTSESTAALCCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 1 ASTKGSVPFLAPCSRSTSESTAALCCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
Db 61 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
QY 123 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 182
Db 121 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 180
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242
Db 181 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 240
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
Db 241 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 300
QY 303 NVFSCSVMEALHNHYTQKSLSLGK 329
Db 301 NVFSCSVMEALHNHYTQKSLSLGK 327

RESULT 2

US-09-313-942-12
; Sequence 12, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-12

Query Match 99.4%; Score 1743; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 7.8e-158;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
Db 3 ASTKGPSVFPAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
Db 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
QY 123 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 182
Db 123 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 182
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242
Db 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
Db 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
QY 303 NVFSCSVMEALHNHYTQKSLSLGK 329
Db 303 NVFSCSVMEALHNHYTQKSLSLGK 329

RESULT 3
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-13152-4

Query Match 99.4%; Score 1743; DB 5; Length 443;

Best Local Similarity 100.0%; Pred. No. 1.2e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASTKGPSVFPAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 62
Db 117 ASTKGPSVFPAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 176
QY 63 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
Db 177 GLYSLSSVTVFPSSSLGKTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 236
QY 123 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 182
Db 237 FLFPKPXTLMISRTPEVTCVVDVDSQEDPEVQFNWYDGVVHNAKTPRREQFNSTY 296
QY 183 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 242
Db 297 RVVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 356
QY 243 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 302
Db 357 NOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPVLDSDGSPFLYSRLTVDKSRWQEG 416
QY 303 NVFSCSVMEALHNHYTQKSLSLGK 329

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Db 417 NVFSCVMHEALHNHYTKSLSLGK 443
|||||
RESULT 4
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-81
Query Match 99.4%; Score 1743; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPFLGGPSV 122
Db 201 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPFLGGPSV 260
Qy 123 FLPPPKDGLMISRTPEVTCVVVDVSDPEQFNWYVDGVEVHNAKTKPREEQFNSTY 182
Db 261 FLPPPKDGLMISRTPEVTCVVVDVSDPEQFNWYVDGVEVHNAKTKPREEQFNSTY 320
Qy 183 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 242
Db 321 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 380
Qy 243 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 302
Db 417 NVFSCVMHEALHNHYTKSLSLGK 443
|||||
RESULT 5
US-08-523-894-8
; Sequence 8, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reiff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-523-894-8
Query Match 99.4%; Score 1743; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGPSVFLPACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPFLGGPSV 122
Db 201 GLYSLSSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPFLGGPSV 260
Qy 123 FLPPPKDGLMISRTPEVTCVVVDVSDPEQFNWYVDGVEVHNAKTKPREEQFNSTY 182
Db 261 FLPPPKDGLMISRTPEVTCVVVDVSDPEQFNWYVDGVEVHNAKTKPREEQFNSTY 320
Qy 183 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 242
Db 321 RVSVSLTVLHODWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPRPQVYVTLPPSQEEMTK 380
Qy 243 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 302
Db 381 NVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSLRTVDKSRWQEG 440
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Db 441 NVFSCVMHEALHNYTKSLSLGK 467
RESULT 7
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12
Query Match 98.7%; Score 1731; DB 3; Length 467;
Best Local Similarity 99.4%; Pred. No. 1.8e-156;
Matches 325; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFEGGPSV 122
Db 201 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFEGGPSV 260
Qy 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDPDPEVQFNWYVDGVVHNATKPREQFNSTY 182
Db 261 FLFPPKPKDTLMISRTPEVTCVVVDVSDPDPEVQFNWYVDGVVHNATKPREQFNSTY 320
Qy 183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPQPREPQVYTLPPSQEEMTK 242
Db 321 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPQPREPQVYTLPPSQEEMTK 380
Qy 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 440
Qy 303 NVFSCVMHEALHNYTKSLSLGK 329
Db 441 NVFSCVMHEALHNYTKSLSLGK 467

Qy 303 NVFSCVMHEALHNYTKSLSLGK 329
Db 441 NVFSCVMHEALHNYTKSLSLGK 467
RESULT 6
US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-10
Query Match 99.0%; Score 1736; DB 3; Length 467;
Best Local Similarity 99.7%; Pred. No. 6.2e-157;
Matches 326; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 62
Db 141 ASTKGSPVPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNWSGALTSGVHTFPAVLQSS 200
Qy 63 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFEGGPSV 122
Db 201 GLYSLSVVTVFSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPFEGGPSV 260
Qy 123 FLFPPKPKDTLMISRTPEVTCVVVDVSDPDPEVQFNWYVDGVVHNATKPREQFNSTY 182
Db 261 FLFPPKPKDTLMISRTPEVTCVVVDVSDPDPEVQFNWYVDGVVHNATKPREQFNSTY 320
Qy 183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPQPREPQVYTLPPSQEEMTK 242
Db 321 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAQGPQPREPQVYTLPPSQEEMTK 380
Qy 243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 302
Db 381 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEG 440
Qy 303 NVFSCVMHEALHNYTKSLSLGK 329

RESULT 8

US-07-916-098A-45
 ; Sequence 45, Application US/07916098A
 ; Patent No. 5871732
 ; GENERAL INFORMATION:
 ; APPLICANT: BURKLY, LINDA C.
 ; APPLICANT: CHISHOLM, PATRICIA L.
 ; APPLICANT: THOMAS, DAVID W.
 ; APPLICANT: ROSA, MARGARET D.
 ; APPLICANT: ROSA, JOSEPH J.
 ; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 ; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 ; STREET: 10 SOUTH WACKER DRIVE
 ; CITY: CHICAGO
 ; STATE: ILLINOIS
 ; COUNTRY: U.S.A.
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07916,098A
 ; FILING DATE: July 24, 1992
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/08843
 ; FILING DATE: No. 5871732ember 27, 1991
 ; CLASSIFICATION: 424
 ; APPLICATION NUMBER: 07/618,542
 ; FILING DATE: No. 5871732ember 27, 1990
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: JOHN J. MC DONNELL
 ; REGISTRATION NUMBER: 26,949
 ; REFERENCE/DOCKET NUMBER: 92.310-G
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 715-1000
 ; TELEFAX: (312) 715-1234
 ; TELEX: 910/221-5317
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 467 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-916-098A-45

Query Match 98.4%; Score 1726.5; DB 2; Length 467;
 Best Local Similarity 99.7%; Pred. No. 58-156; 0; Mismatches 0; Indels 1; Gaps 1;
 Matches 326; Conservative 0;
 QY 3 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 62
 DB 142 ASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 201
 QY 63 GLYSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPAPCFELGGPSV 122
 DB 202 GLYSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPAPCFELGGPSV 261
 QY 123 FLPPPPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNATKPREEOFNST 182
 DB 262 FLPPPPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNATKPREEOFNST 321
 QY 183 RVVSVLTVLHQDLNKGKVKVSKNGLPSSIEKTSIKAKGPRFPQVYTLPPSQEEMTK 242
 DB 322 RVVSVLTVLHQDLNKGKVKVSKNGLPSSIEKTSIKAK-QPRFPQVYTLPPSQEEMTK 380

QY 243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPFVLDSDGSGFFLYSLTVDKSRWQEG 302
 DB 381 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPFVLDSDGSGFFLYSLTVDKSRWQEG 440
 QY 303 NVFSCSVMEALHNHYTQKSLSLGLK 329
 DB 441 NVFSCSVMEALHNHYTQKSLSLGLK 467
 RESULT 9
 US-08-477-460B-4
 ; Sequence 4, Application US/08477460B
 ; Patent No. 6034223
 ; GENERAL INFORMATION:
 ; APPLICANT: Progenics Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
 ; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-1gG2 IMMUNOCONJUGATES, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,460B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/927,931
 ; FILING DATE: 07-AUG-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JFW/AJM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 977-9550
 ; TELEFAX: (212) 977-9809
 ; TELEX: 422523 COOP UI
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 530 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CONA
 ; ORIGINAL SOURCE:
 ; ORGANISM: homo sapien
 ; CELL TYPE: lymphocyte
 ; US-08-477-460B-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;
 Best Local Similarity 92.4%; Pred. No. 5-4e-145;
 Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
 QY 2 FASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 61
 DB 204 FASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 263
 QY 62 SGYLSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPAPCFELGGPS 121
 DB 264 SGYLSLSVVTVPSSSLGTYTCNVVDHSPNTKVDKRVESKYGPCCPAPCFELGGPS 322
 QY 122 VFLPPPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNATKPREEOFNST 181
 DB 323 VFLPPPKDTLMISRTPEVTCVVDVSQEDPEVQFNWYVDGVEVHNATKPREEOFNST 382

182 YRVSVLTCLVHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241
383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442
242 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301
443 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502
302 GNVFSCVMHEALHNHYTKQSLSLGK 329
503 GNVFSCVMHEALHNHYTKQSLSLSPGK 530

RESULT 10
US-08-379-516-4
; Sequence 4, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; TITLE OF INVENTION: Immunoconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 61
Db 204 FASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 263
QY 62 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKVESKYGPPCPCPAPFLGQPS 121
Db 264 SGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKVERKCCVCEPCPAPP-VAGPS 322
QY 122 VLFPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVVHNAKTKPREEQFNST 181
Db 323 VLFPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVVHNAKTKPREEQFNST 382
QY 182 YRVSVLTCLVHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241
Db 383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442
QY 242 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301
Db 443 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502
302 GNVFSCVMHEALHNHYTKQSLSLGK 329
503 GNVFSCVMHEALHNHYTKQSLSLSPGK 530

RESULT 11
US-09-329-916-4
; Sequence 4, Application US/09329916
; Patent No. 617549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.

182 YRVSVLTCLVHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241
383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442
242 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301
443 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502
302 GNVFSCVMHEALHNHYTKQSLSLGK 329
503 GNVFSCVMHEALHNHYTKQSLSLSPGK 530

RESULT 10
US-08-379-516-4
; Sequence 4, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allway, Graham P.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; TITLE OF INVENTION: Immunoconjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; CURRENT FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; EARLIER FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 61
Db 204 FASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 263
QY 62 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKVESKYGPPCPCPAPFLGQPS 121
Db 264 SGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKVERKCCVCEPCPAPP-VAGPS 322
QY 122 VLFPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVVHNAKTKPREEQFNST 181
Db 323 VLFPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVVHNAKTKPREEQFNST 382
QY 182 YRVSVLTCLVHODWLNKGYKCKVSNKGLPSSIEKTSKAGOPRPPQVYTLPPSOEEMT 241
Db 383 FRVSVLTVVHODWLNKGYKCKVSNKGLPAPIEKTSKAGOPRPPQVYTLPPSOEEMT 442
QY 242 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 301
Db 443 KQVSLTCLVKGFPSPDIWESNGQPNENYKTPPVLDSDGSGFFLYSLRTVDKSRWQE 502
302 GNVFSCVMHEALHNHYTKQSLSLGK 329
503 GNVFSCVMHEALHNHYTKQSLSLSPGK 530

RESULT 12
US-08-485-372A-4
; Sequence 4, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1195 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-485-372A-4

Query Match 91.9%; Score 1611.5; DB 3; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 61
DB 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 263
QY 62 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 121
DB 264 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 322
QY 122 VFLFPKPKDLMISRTPEVTCVVDVSDQEPVQFNWYDGVVHNATKPREEQFNST 181
DB 323 VFLFPKPKDLMISRTPEVTCVVDVSDQEPVQFNWYDGVVHNATKPREEQFNST 382
QY 182 YRVVSVLTVLHODWLNKGYCKVSKNGLPSPISIEKTSKAKGQPREPQVYTLPPSQEEMT 241
DB 383 FRVSVLTVWHDWLNKGYCKVSKNGLPAPIEIKTSKTKGQPREPQVYTLPPSQEEMT 442
QY 242 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 301
DB 443 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 502
QY 302 GNVFCSVMHEALHNHYTQKSLSLIGK 329

DB 503 GNVFCSVMHEALHNHYTQKSLSLSPGK 530
RESULT 13
US-09-409-006A-4
; Sequence 4, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOISTY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,006A
; FILING DATE: 23-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-409-006A-4

Query Match 91.9%; Score 1611.5; DB 4; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 61
DB 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 263
QY 62 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 121
DB 264 SGLYSLSSVTVVPSNFGTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGQPS 322
QY 122 VFLFPKPKDLMISRTPEVTCVVDVSDQEPVQFNWYDGVVHNATKPREEQFNST 181
DB 323 VFLFPKPKDLMISRTPEVTCVVDVSDQEPVQFNWYDGVVHNATKPREEQFNST 382
QY 182 YRVVSVLTVLHODWLNKGYCKVSKNGLPSPISIEKTSKAKGQPREPQVYTLPPSQEEMT 241
DB 383 FRVSVLTVWHDWLNKGYCKVSKNGLPAPIEIKTSKTKGQPREPQVYTLPPSQEEMT 442
QY 242 KQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFPLYSLRTVDKSRWQE 301

Db 443 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPMLDSGSGFFLYSKLTVDKSRWQ 502
QY 302 GNVFSCSVNHEALHNHYTKSLSLGLK 329
Db 503 GNVFSCSVNHEALHNHYTKSLSLSPGK 530

RESULT 14

US-08-484-681-4
; Sequence 4, Application US/08484681
; Patent No. 6451313
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,681
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-484-681-4

Query Match 91.9%; Score 1611.5; DB 4; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145; Indels 1; Gaps 1;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61
Db 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263
QY 62 SGYLSLVSVVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKVGPPCPSCPAPEFLGGPS 121
Db 264 SGYLSLVSVVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKVGPPCPSCPAPEFLGGPS 322
QY 122 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWTVDGVVEVHNATKPREEQFNST 181
Db 323 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWTVDGVVEVHNATKPREEQFNST 382
QY 182 YRVVSVLTVLHQDWLNGKEYCKVSNKGLPAPIEKTIISKAKQGPPEPQVYTLPPSQEEMT 241
Db 383 FRVVSVLTVHQDWLNGKEYCKVSNKGLPAPIEKTIISKAKQGPPEPQVYTLPPSQEEMT 442

QY 242 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 301
Db 443 KNOVSLTCLVKGFPDIAVWESNGQPENNYKTTTPMLDSGSGFFLYSKLTVDKSRWQ 502
QY 302 GNVFSCSVNHEALHNHYTKSLSLGLK 329
Db 503 GNVFSCSVNHEALHNHYTKSLSLSPGK 530

RESULT 15

PCT-US93-07422-4
; Sequence 4, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07422
; FILING DATE: 19930806
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
PCT-US93-07422-4

Query Match 91.9%; Score 1611.5; DB 5; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145; Indels 1; Gaps 1;
Matches 303; Conservative 10; Mismatches 14; Indels 1; Gaps 1;
QY 2 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 61
Db 204 FASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 263
QY 62 SGYLSLVSVVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKVGPPCPSCPAPEFLGGPS 121
Db 264 SGYLSLVSVVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKVGPPCPSCPAPEFLGGPS 322
QY 122 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWTVDGVVEVHNATKPREEQFNST 181
Db 323 VFLFPPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWTVDGVVEVHNATKPREEQFNST 382
QY 182 YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKQGPPEPQVYTLPPSQEEMT 241

Db	383	FRVSVLTVHODWLNKGYKCKVSNKGLPAPTEXTISKTKQPREQVYTLPPSREMT	442
Qy	242	KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLLTVDKSRWQE	301
Db	443	KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPMLDSDGSGFFLYSKLTVDKSRWQQ	502
Qy	302	GNVFCSVMHEALHNHYTQKSLSLSPGK	329
Db	503	GNVFCSVMHEALHNHYTQKSLSLSPGK	530

Search completed: January 13, 2004, 12:46:36
Job time : 29.4463 secs


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Db      50 HISPYNQATTYNQNF 65

RESULT 3
S17604
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000.
C:Accession: S17604
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17604
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <L>A>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 98;
Best Local Similarity 62.5%; Pred. No. 0.043;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNQITTYDQNLKG 17
       |:|||||:|:|:|
Db      44 INPYNGDTFYNQKPKG 59

RESULT 4
S26320
IG heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S26320
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26320
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59206
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 0.047;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 IDPYNQITTYDQNLK 16
       |:|||||:|:|:|
Db      39 INPYNGATSYNQNF 53

RESULT 5
S26319
IG heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26319
A:Molecule type: mRNA
A:Residues: 1-114 <STA>
A:Cross-references: EMBL:X59172
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 114;
Best Local Similarity 62.5%; Pred. No. 0.05;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNQITTYDQNLKG 17
       |:|||||:|:|:|
Db      47 INPYNGDTFYNQKPKG 62

RESULT 6
PS0057
IG heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: PS0057
R:Yasota, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy
A:Reference number: PS0057; MUID:89197817; PMID:2467902
A:Accession: PS0057
A:Molecule type: DNA
A:Residues: 1-135 <YAO>
A:Cross-references: GB:D00307; NID:9220448; PIDN:BAA00213.1; PID:9220449
A:Note: The authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gl.
C:Comment: The gene encoding this protein was isolated from a hybridoma that produces a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 135;
Best Local Similarity 62.5%; Pred. No. 0.061;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IDPYNQITTYDQNLKG 17
       |:|||||:|:|:|
Db      70 INPYNGDTFYNQKPKG 85

RESULT 7
A27609
IG heavy chain precursor V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A:Reference number: A27609; MUID:88154467; PMID:3126234
A:Accession: A27609
A:Molecule type: DNA
A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:M19401; NID:9195441; PIDN:AAA38303.1; PID:9553992
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      60.0%; Score 57; DB 2; Length 139;
Best Local Similarity 58.8%; Pred. No. 0.063;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YIDPYNQITTYDQNLKG 17
       |:|||||:|:|:|
Db      69 YINPYNDYTSYNQKPKG 85
```


R:Berdoz, J.; Krachenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A:Description: Specific amplification by the polymerase chain reaction of rearranged genes
A:Reference number: S52445
A:Accession: S52445
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <BER>
A:Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-115/Domain: immunoglobulin homology <IMM>

QY 2 IDPYNGITTYDQNLKG 17
DB 43 IDPESGGTAYNQNFPG 58

Search completed: January 13, 2004, 12:44:44
Job time : 2.23231 secs

Query Match 55.8%; Score 53; DB 2; Length 137;
Best Local Similarity 52.9%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
DB 59 WIDPENGNTYIDPKFQG 85

RESULT 14
A37263
Ig heavy chain V region (4A9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 16-Aug-1996
C:Accession: A37263
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: A37263
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57996
A:Note: the authors translated the codon CAA for residue 38 as His, AGA for residue 39 as
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 54.7%; Score 52; DB 2; Length 93;
Best Local Similarity 52.5%; Pred. No. 0.26;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITTYDQNLKG 17
DB 35 IDPQGGTAYNQNFPG 50

RESULT 15
I37262
Ig heavy chain V region (1G1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: I37262
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: I37262
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-101 <GOS>
A:Cross-references: GB:M57995; NID:g195375; PIDN:AA63334.1; PID:g195376
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 54.7%; Score 52; DB 2; Length 101;
Best Local Similarity 52.5%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

RA Viari A., Wamburt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
RT Nature 390:249-256 (1997).
RL -1- FUNCTION: NOT KNOWN.
CC -1- SIMILARITY: BELONGS TO THE FLIT FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
EMBL; Z31376; CAA93250.1; -;
DR EMBL; U56901; AAC44955.1; -;
DR EMBL; Z59122; CAB15549.1; -;
DR PIR; I40399; I40399.
DR Subtilist; BG10923; flit.
KW Flagella; Complete proteome.
SQ SEQUENCE 113 AA; 13536 MW; 5AA78802EBDBA88E CRC64;
Query Match 47.4%; Score 45; DB 1; Length 113;
Best Local Similarity 52.9%; Pred. No. 2.2;
Matches 9; Conservative 3; Mismatches 1; Indels 4; Gaps 1;
QY 1 YIDPYNGITI-----YDQ 13
DB 95 YLNPYNNITIDGTYYDK 111
RESULT 6
HW12 MOUSE
ID HW12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region MOPC 104E.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehy M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.S.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424 (1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02039; MHMS4E.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; Igv, 1.
DR PROSITE; PS50835; IG_Like; 1.
DR Immunoglobulin V region; Glycoprotein.
KW DOMAIN 1 116
FT DISULFID 22 96 IG-LIKE.
FT CARBOHYD 55 55 BY SIMILARITY.
FT NON_TER 117 117 N-LINKED (GLCNAC...) (COMPLEX).
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

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Query Match      47.4%; Score 45; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 IDPYNGITIYDQNLKG 17
DB      51 INPNNGGTSYNQKFKG 66

RESULT 7
HV13 MOUSE
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A36242; MHM5J5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON TER 118 118
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match      47.4%; Score 45; DB 1; Length 117;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 IDPYNGITIYDQNLKG 17
DB      51 INPNNGGTSYNQKFKG 66

RESULT 8
HV51 MOUSE
ID HV51 MOUSE STANDARD; PRT; 118 AA.
AC P06370;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B

```

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RT Lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J_3-517-523(1984).
DR PIR; A02040; MHM38.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match      47.4%; Score 45; DB 1; Length 118;
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 IDPYNGITIYDQNLKG 17
DB      51 INPNNGGTSYNQKFKG 66

RESULT 9
VL1 HPVME
ID VL1 HPVME STANDARD; PRT; 505 AA.
AC P27564;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major capsid protein L1.
GN L1.
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180.";
RL J. Virol. 65:5564-5568(1991).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73258; AAF14010.1; -.
DR PIR; B40509; P1WLPR.
DR InterPro; IPR002210; PV capsid_L1.
DR Pfam; PF00500; late protein_L1; 1.
DR PRINTS; PR00865; HPVcapsidL1.
DR ProDom; PD000544; PV_capsid_L1; 1.
KW Coat protein; late protein.
SQ SEQUENCE 505 AA; 56805 MW; 595DE493B708207B CRC64;

Query Match      47.4%; Score 45; DB 1; Length 505;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      3 DPYNGITIIDQNLK 16
DB      440 DPYDGLNFMVNLK 453

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RESULT 10
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=A/J;
RC MEDLINE=82152618; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00493; AAA38128.1; -
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FEJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE3 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 140;
Best Local Similarity 47.1%; Pred. NO. 4;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17
DB 69 YINPGNGYINYEKPKG 85

RESULT 11
Y094 CAEEL
ID Y094 CAEEL STANDARD; PRT; 335 AA.
AC F41844;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 40.1 kDa protein T20B12.4 in chromosome III.
GN T20B12.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
```

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Waterston R.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: STRONG, TO C.ELEGANS K06H7.2.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; U10401; AAA19057.1; -
DR PIR; T16904; T16904.
DR WormPep; T20B12.4; CE01410.
KW Hypothetical protein.
SQ SEQUENCE 335 AA; 40139 MW; 9DE51B219062B8E7 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 335;
Best Local Similarity 80.0%; Pred. NO. 10;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDPYNGITIV 11
DB 298 IDPYESITIV 307

RESULT 12
PMBE ECOLI
ID PMBE ECOLI STANDARD; PRT; 450 AA.
AC P24231;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 18-OCT-2001 (Rel. 40, Last annotation update)
DE PMBA protein (Tlde protein).
GN PMBA OR TLDE OR B4235 OR Z5845 OR ECS5212.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91186828; PubMed=2082149;
RA Rodriguez-Sainz M.C., Hernandez-Chico C., Moreno F.;
RT "Molecular characterization of pmBA, an Escherichia coli chromosomal
RT gene required for the production of the antibiotic peptide MccB17."
RL Mol. Microbiol. 4:1921-1932(1990).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=K12;
RX MEDLINE=96177756; PubMed=8604133;
RA Murayama N., Shimizu H., Takiguchi S., Baba Y., Amino H.,
RA Horiuchi T., Sekimizu K., Miki T.;
RT "Evidence for involvement of Escherichia coli genes pmBA, csrA and a
RT previously unrecognized gene tldD, in the control of DNA gyrase by
RT lsdD (ccdB) of sex factor F."
RL J. Mol. Biol. 256:483-502(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
```


QY 3 DPYNGITTYDQNLK 16
 Db 437 DRYAGLSFEVNLK 450

RESULT 15

RPD_GUITH STANDARD; PRT: 1286 AA.
 AC 078483;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA-directed RNA polymerase beta" Chain (EC 2.7.7.6).
 GN RPOC2.
 OS Guillardia theta (Cryptomonas phi).
 OG Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=55529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99128221; PubMed=99299392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, Guillardia theta:
 RT complete sequence and conserved synteny groups confirm its common
 RT ancestry with red algae.";
 RL J. Mol. Evol. 48:236-244(1999).
 CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
 CC subunits: alpha, beta, beta', and beta".
 CC
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 CC
 CC EMBL; AF041468; AAC35674.1; -.
 DR HSP; Q9KMU6; 1HQW.
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR InterPro; IPR007081; RNA_pol_Rpb1_5.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpb1_5; 2.
 KW Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
 SQ SEQUENCE 1286 AA; 145044 MW; BEFF46PEF5522C73 CRC64;
 Query Match 46.3%; Score 44; DB 1; Length 1286;
 Best Local Similarity 61.5%; Pred. NO. 44;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 PYNGITTYDQNLK 16
 Db 363 PFNGIIRYKVLK 375

Search completed: January 13, 2004, 12:39:32
 Job time : 3.74236 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:20:44 ; Search time 3.04367 Seconds
(without alignments)
1441.318 Million cell updates/sec

Title: US-09-990-586-101

Perfect score: 95

Sequence: 1 YIDPYNGITTYDQNLKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23: *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	65.3	481	11 Q8VCV5	Q8VCV5 mus musculus
2	54	56.8	488	11 Q91WR1	Q91WR1 mus musculus
3	51	53.7	120	11 Q920E8	Q920E8 mus musculus
4	51	53.7	148	12 Q11401	Q11401 reindeer pa
5	50	52.6	109	11 Q9JL75	Q9JL75 mus musculus
6	48	50.5	243	17 Q28486	Q28486 archaeglob
7	47.5	50.0	954	5 Q8IC07	Q8IC07 plasmodium
8	47	49.5	481	11 Q91WT3	Q91WT3 mus musculus
9	47	49.5	595	16 Q8VCE9	Q8VCE9 anabaena sp
10	46	48.4	385	16 Q9PQ56	Q9PQ56 ureaplasma
11	46	48.4	675	10 Q9FNM5	Q9FNM5 arabidopsis
12	46	48.4	681	10 Q8RWP3	Q8RWP3 arabidopsis
13	45	47.4	117	11 Q9QXE9	Q9QXE9 mus musculus
14	45	47.4	117	11 Q9QXF0	Q9QXF0 mus musculus
15	45	47.4	152	12 Q81070	Q81070 human papil
16	45	47.4	152	12 Q9WIV1	Q9WIV1 human papil

17	45	47.4	238	5 Q17518	Q17518 caenorhabdi
18	45	47.4	501	12 Q8BDQ8	Q8BDQ8 reindeer pa
19	45	47.4	1092	8 Q8HTL4	Q8HTL4 chlamydomon
20	44	46.3	170	17 Q96XK1	Q96XK1 sulfolobus
21	44	46.3	223	2 Q50398	Q50398 mycoplasma
22	44	46.3	261	16 Q8UB53	Q8UB53 agrobacteri
23	44	46.3	450	16 Q8XGJ7	Q8XGJ7 salmonella
24	44	46.3	450	16 Q8FAP2	Q8FAP2 escherichia
25	44	46.3	501	12 Q37391	Q37391 common chim
26	44	46.3	889	10 Q9FXA5	Q9FXA5 arabidopsis
27	44	46.3	897	10 Q9C7W9	Q9C7W9 arabidopsis
28	44	46.3	938	16 Q8FP27	Q8FP27 corynebacte
29	44	46.3	1007	10 Q9C7X0	Q9C7X0 arabidopsis
30	44	46.3	3574	5 Q8IDA8	Q8IDA8 plasmodium
31	43.5	45.8	403	16 Q8DZW4	Q8DZW4 wiggleswort
32	43	45.3	162	2 Q93SR7	Q93SR7 pseudomonas
33	43	45.3	162	16 Q910W5	Q910W5 pseudomonas
34	43	45.3	580	12 Q91LH9	Q91LH9 white spot
35	43	45.3	581	12 Q8VB97	Q8VB97 white spot
36	43	45.3	607	16 Q8CY30	Q8CY30 brucella su
37	43	45.3	775	16 Q8XNT7	Q8XNT7 clostridium
38	43	45.3	878	16 Q8P6M3	Q8P6M3 xanthomonas
39	43	45.3	2110	5 Q8IB35	Q8IB35 plasmodium
40	42	44.2	119	5 Q9GY22	Q9GY22 schistosoma
41	42	44.2	151	12 Q84227	Q84227 human papil
42	42	44.2	364	2 Q93QW3	Q93QW3 bacteroides
43	42	44.2	476	17 Q97XC8	Q97XC8 sulfolobus
44	42	44.2	482	12 Q91HD9	Q91HD9 bovine herp
45	42	44.2	503	12 Q99FW7	Q99FW7 human papil

ALIGNMENTS

RESULT 1

Q8VCV5 PRELIMINARY; PRT; 481 AA.
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018455; AAH18455.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_LV.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 65.3%; Score 62; DB 11; Length 481;

Best Local Similarity 64.7%; Pred. NO. 0.18; Mismatches 4; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17

DB 69 YIDPYNGSSYNQKFKG 85

RESULT 2

Q91WR1


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FT NON TER 109 109
SQ SEQUENCE 109 AA; 12118 MW; FF65B441BBF936A6 CRC64;

Query Match 52.6%; Score 50; DB 11; Length 109;
Best Local Similarity 52.9%; Pred. No. 2; 9; Mismatches 0; Gaps 0;
Matches 9; Conservative 3; Indels 5;

QY 1 YIDPYNGITTYDQNLKG 17
|||::|:|:|
Db 41 YINPYNDGTNYNEKFKG 57

RESULT 6
O28486 PRELIMINARY; PRT; 243 AA.
AC O28486;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Methylthioadenosine phosphorylase (MTAP).
GN AF1788.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton P.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AB000979; AAB89459.1; -.
DR HSP; Q13126; 1CB0.
DR TIGR; AF1788; -.
DR InterPro; IPR001369; Map_PNP.
DR Pfam; PF00896; Map_PNP; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 243 AA; 27201 MW; C8FCFE74DAC89DCC CRC64;

Query Match 50.5%; Score 48; DB 17; Length 243;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNL 15
|||::|:|:|
Db 101 YIDFFSGVTYNDLSL 115

RESULT 7
Q81C07 PRELIMINARY; PRT; 954 AA.
AC Q81C07;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PF07_0028.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]

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RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844506; CAD50834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 954 AA; 115329 MW; 25417952D67DD6C4 CRC64;

Query Match 50.0%; Score 47.5; DB 5; Length 954;
Best Local Similarity 52.6%; Pred. No. 72;
Matches 10; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 YIDPYNG---ITTYDQNLK 16
|||::|:|:|
Db 462 YIQPHNGIHHITNYKQNR 480

RESULT 8
Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.0 kDa protein.
GN IGH-VJ558 OR AI891585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAH3488.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4BEB5C253038B718 CRC64;

Query Match 49.5%; Score 47; DB 11; Length 481;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITTYDQNLKG 17
|||::|:|:|
Db 70 IDFFPSYTSYNQKPKG 85

RESULT 9
Q8YQ89 PRELIMINARY; PRT; 595 AA.
AC Q8YQ89;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Periplasmic oligopeptide-binding protein of oligopeptide ABC
DE transporter.
GN ALR3884.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

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RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.,
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium *Anabaena* sp. strain PCC 7120.",
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003594; BAB75583.1; -;
 DR InterPro; IPR000914; SBP_bac_5.
 DR Pfam; PF00496; SBP_bac_5; 3.
 KW Complete proteome.
 SQ SEQUENCE 595 AA; 67165 MW; D7070EBA85F0D17 CRC64;

Query Match 49.5%; Score 47; DB 16; Length 595;
 Best Local Similarity 43.8%; Pred.No. 53;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLK 16
 | : : : : :
 DB 379 YLSPEGLKVIDYNLE 394

RESULT 10
 Q9PQ56 PRELIMINARY; PRT; 386 AA.
 ID Q9PQ56
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Serine/threonine kinase.
 GN PKN OR U0216.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Serovar 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen *Ureaplasma*
 RT *urealyticum*.",
 RL Nature 407:757-762(2000).
 DR EMBL; AE002120; AAF30624.1; -;
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferase; Complete proteome.
 SQ SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;

Query Match 48.4%; Score 46; DB 16; Length 386;
 Best Local Similarity 52.9%; Pred.No. 48;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLK 17
 | : : : : :
 DB 326 YIKPLNKLIRYKNLAG 342

RESULT 11
 Q9FNMS PRELIMINARY; PRT; 675 AA.
 ID Q9FNMS
 AC Q9FNMS;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE GTP-binding protein LepA homolog
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=98069011; PubMed=9405937;
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones.",
 RL DNA Res. 4:291-300(1997).
 DR EMBL; AB066697; BAB10014.1; -;
 DR HSSP; F13551; 1DAR.
 DR InterPro; IPR000640; EFG_C.
 DR InterPro; IPR004161; EFTU_D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR006297; LepA.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF06679; ERG_C; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU_D2; 1.
 DR PRINTS; PR00315; ELONGATNFCT.
 DR TIGRFAMs; TIGR01393; LepA; 1.
 DR TIGRFAMs; TIGR02231; small_GTP; 1.
 DR PROSITE; PS00301; EFATOR_GTP; 1.
 KW GTP-binding; Protein biosynthesis.
 SQ SEQUENCE 675 AA; 74874 MW; 824A3D0B093497E5 CRC64;

Query Match 48.4%; Score 46; DB 10; Length 675;
 Best Local Similarity 41.2%; Pred.No. 87;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLK 17
 | : : : : :
 DB 274 YIDPYRGVIVYFRVIDG 290

RESULT 12
 Q8RWP3 PRELIMINARY; PRT; 681 AA.
 ID Q8RWP3
 AC Q8RWP3
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE GTP-binding protein LepA-like protein.
 GN AT5G08650.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY029258; AAM12957.1; -;
 DR EMBL; AY128719; AAM91119.1; -;
 DR InterPro; IPR000640; EFG_C.

DR InterPro; IPR004161; EFTU D2.
 DR InterPro; IPR000795; EF_GTPbind.
 DR InterPro; IPR006297; LepA.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00679; ERG_C; 1.
 DR Pfam; PF00009; GTP_EFTU; 1.
 DR Pfam; PF03144; GTP_EFTU D2; 1.
 DR TIGRFAMs; TIGR01393; lepA; 1.
 DR TIGRFAMs; TIGR00231; small_GTP; 1.
 DR PROSITE; PS00301; EFACOR_GTP; 1.
 KW GTP-binding; Protein biosynthesis.
 SQ SEQUENCE 681 AA; 75424 MW; 0C850E50DC5B9C4C CRC64;

Query Match 48.4%; Score 46; DB 10; Length 681;
 Best Local Similarity 41.2%; Pred. No. 87;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDQNLKG 17
 |||||:|:|:|
 Db 280 YIDPYRGVIVFVIDG 296

RESULT 13

Q9QXE9 PRELIMINARY; PRT; 117 AA.
 AC Q9QXE9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 23, Last annotation update)
 DE Immunoglobulin heavy chain V-D-J region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225174; CAB65237.1; -.
 DR HSSP; P01810; 2FBJ

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 47.4%; Score 45; DB 11; Length 117;
 Best Local Similarity 56.2%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITIVDQNLKG 17
 |||||:|:|:|
 Db 51 INPNNGGTSYNQKFKG 66

RESULT 14

Q9QXF0 PRELIMINARY; PRT; 117 AA.
 AC Q9QXF0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 23, Last annotation update)
 DE Immunoglobulin heavy chain V-D-J region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ225174; CAB65236.1; -.
 DR HSSP; P01789; 1MCP.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 117
 SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 47.4%; Score 45; DB 11; Length 117;
 Best Local Similarity 56.2%; Pred. No. 20;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IDPYNGITIVDQNLKG 17
 |||||:|:|:|
 Db 51 INPNNGGTSYNQKFKG 66

RESULT 15

Q81070 PRELIMINARY; PRT; 152 AA.
 AC Q81070;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Major capsid protein L1 (Fragment).
 OS Human.
 GN Human papillomavirus type 68.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus
 OX NCBI_TaxID=45240;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=IS362;
 RX MEDLINE=96186743; PubMed=8627792;
 RA Stewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
 Peto J., Wheeler C.M.;
 RT "Intratype variation in 12 human papillomavirus types: a worldwide
 perspective.";
 RL J. Virol. 70:3127-3136 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=IS362;
 RA Farmer A.D.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U45934; AAB19169.1; -.
 DR InterPro; IPR002210; PV_capsid_L1.
 DR Pfam; PF00500; late_protein_L1; 1.
 DR PRINTS; PR00865; HPVcapsidL1.
 DR ProDom; PD000544; PV_capsid_L1; 1.
 FT NON_TER 1
 FT NON_TER 152
 SQ SEQUENCE 152 AA; 17331 MW; CCF76574491F7D2D CRC64;

Query Match 47.4%; Score 45; DB 12; Length 152;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 DPYNGITIVDQNLK 16
 |||||:|:|:|
 Db 125 DPYDGLNFWNVNLK 138

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
680.681 Million cell updates/sec

Title: US-09-990-586-101

Perfect score: 95

Sequence: 1 YIDPYNGITTYDQNLKG 17

Scoring table: BLOSUM62

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	95.8	17	AAW71859	Human anti-tissue
2	91	95.8	17	AAW71288	Human anti-tissue
3	72	75.8	118	AAV52755	Anti-tissue factor
4	72	75.8	118	AAV52756	Anti-tissue factor
5	69	72.6	110	AAW84059	Vitronectin alpha
6	69	72.6	117	AAW84093	Murine vitronectin
7	69	72.6	117	AAW84097	Humanised anti-alp
8	62	65.3	116	AAW22418	Reshaped human AUK
9	62	65.3	135	AAW29016	pUC-RVh-1220b. Sy

10	62	65.3	135	13	AAW29017	pUC-RVh-1220d. Sy
11	62	65.3	135	13	AAW28669	p12-h2. Synthetic
12	62	65.3	214	24	ABP96759	TSH receptor antib
13	62	65.3	214	24	ABP96760	TSH receptor antib
14	60	63.2	119	14	AAW34570	VH Fv fragment of
15	60	63.2	119	14	AAW38586	Anti-digoxin monocl
16	60	63.2	119	22	AAW62294	Murine monoclonal
17	60	63.2	121	9	AAW81363	Heavy chain variab
18	60	63.2	123	22	AAW62298	Murine monoclonal
19	60	63.2	214	24	ABP96763	TSH receptor antib
20	60	63.2	214	24	ABP96764	TSH receptor antib
21	60	63.2	240	9	AAW80153	Binding site. Hom
22	60	63.2	246	13	AAW27245	Sequence of the AA
23	60	63.2	246	14	AAW44229	Chimeric Ig superf
24	60	63.2	251	9	AAW80152	Multifunctional pr
25	60	63.2	252	17	AAW02279	26-10 anti-digoxin
26	60	63.2	252	19	AAW53169	26-10 anti-digoxin
27	60	63.2	252	20	AAW80423	Anti-digoxin sfv
28	60	63.2	260	20	AAW95600	Anti-digoxin scfv
29	60	63.2	260	20	AAW83101	Anti-digoxin singl
30	60	63.2	261	14	AAW44230	Chimeric Ig superf
31	60	63.2	267	14	AAW44227	Chimeric Ig superf
32	60	63.2	269	22	AAW60567	Anti-digoxin singl
33	60	63.2	272	14	AAW34672	26-10 sfv. Synthe
34	60	63.2	274	14	AAW44228	Chimeric Ig superf
35	60	63.2	311	9	AAW80151	Multifunctional pr
36	60	63.2	311	11	AAW05378	Multifunctional pr
37	60	63.2	313	22	AAW62305	Single chain antib
38	60	63.2	367	13	AAW27244	Sequence encoded b
39	59	62.1	117	20	AAW29450	Murine 6G425 heavy
40	59	62.1	117	20	AAW29451	Humanised 6G425 F
41	59	62.1	117	21	AAW30310	Humanised murine 6
42	59	62.1	117	21	AAW30311	Humanised murine 6
43	59	62.1	117	21	AAW77753	Murine 6G425 heavy
44	59	62.1	117	21	AAW77754	Humanised 6G425 F
45	59	62.1	117	24	ABW59500	Mouse antibody 6G4

ALIGNMENTS

RESULT 1
AAW71859
ID AAW71859 standard; peptide; 17 AA.
XX AC AAW71859;
XX AC AAW71859;
DT 10-DEC-1998 (first entry)
XX DE Human anti-tissue factor antibody hypervariable region #5.
XX DE Human anti-tissue factor light chain variable region; H36.D2.B7;
KW Human; anti-tissue factor heavy chain variable region; inhibition; antibody;
KW anti-tissue factor heavy chain variable region; inhibition; antibody;
KW blood coagulation; thrombosis; restenosis; thromboembolic condition;
KW cardiovascular; infection; neoplastic disease; clot; diagnosis.
XX KW
OS Homo sapiens.
XX OS
XX PN WO9840408-A1.
XX PN
XX PD 17-SEP-1998.
XX PD
XX PF 10-MAR-1998; 98WO-US04644.
XX PF
XX PR 10-MAR-1997; 97US-0814806.
XX PR
XX PA (SUNO-) SUNOL MOLECULAR CORP.
XX PA
PI Jiao J, Luepschen L, Nieves EL, Wong HC;
XX Jiao J, Luepschen L, Nieves EL, Wong HC;
DR WPI; 1998-520804/44.
DR Reshaped human AUK
DR N-PSDB; AAW61138.
XX DR

PT New antibody to human tissue factor - used for, e.g. treating
 PT thrombosis or restenosis or thromboembolic conditions associated
 PT with cardiovascular, infectious or neoplastic disease
 XX
 PS
 XX Claim 13; Page 31; 53pp; English.

CC The present sequence represents a hypervariable region from the human
 CC anti-tissue factor antibody that binds native human tissue factor (TF)
 CC and does not bind non-native TF. The antibody capable of specifically
 CC binding native TF may be used for inhibiting blood coagulation and also
 CC for reducing TF levels in a mammal. The antibodies can be used, e.g. to
 CC treat thromboses, particularly to prevent or inhibit restenosis, or
 CC other thromboses, following an invasive medical procedure such as
 CC arterial or cardiac surgery (e.g. angioplasty, endarterectomy,
 CC deployment of a stent, use of catheter, graft implantation or use of an
 CC arteriovenous shunt). The antibodies can also be used as a carrier for
 CC blood clot such as streptokinase, tissue plasminogen activator (t-PA)
 CC or urokinase, or a cytotoxic agent by conjugating a suitable toxin to
 CC the antibody. Further the antibodies can be used for treating a
 CC thromboembolic condition associated with cardiovascular disease, an
 CC infectious disease, a neoplastic disease or as a thrombolytic agent.
 CC The antibodies can also be used for detection and diagnosis.
 XX
 XX Sequence 17 AA;

Query Match 95.8%; Score 91; DB 19; Length 17;
 Best Local Similarity 94.1%; Pred. No. 3.5e-08;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17
 |||||
 DB 1 YIDPYNGITIYDQNFKG 17

RESULT 2
 ID AAW71288 standard; Protein; 117 AA.
 XX
 XX AAW71288;
 AC
 XX
 DT 10-DEC-1998 (first entry)
 XX Human anti-tissue factor heavy chain variable region.
 DE
 XX Human; anti-tissue factor light chain variable region; H36.D2.B7;
 KW anti-tissue factor heavy chain variable region; inhibition; antibody;
 KW blood coagulation; thrombosis; restenosis; thromboembolic condition;
 KW cardiovascular; infection; neoplastic disease; clot; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX WO9840408-A1.
 PN
 XX 17-SEP-1998.
 PD
 XX
 XX 10-MAR-1998; 98WO-US04644.
 PF
 XX
 XX 10-MAR-1997; 97US-0814806.
 PR
 XX (SUNO-) SUNOL MOLECULAR CORP.
 PA
 XX Jiao J, Luepschen L, Nieves EL, Wong HC;
 XX WPI; 1998-520804/44.
 DR N-PSDB; AAV54962.
 DR
 XX New antibody to human tissue factor - used for, e.g. treating
 PT thrombosis or restenosis or thromboembolic conditions associated
 PT with cardiovascular, infectious or neoplastic disease
 XX
 XX Claim 12; Fig 1B; 53pp; English.

CC The present sequence represents the human anti-tissue factor heavy chain
 CC variable region from an antibody that binds native human tissue factor
 CC (TF) and does not bind non-native TF. The antibody capable of
 CC specifically binding native TF may be used for inhibiting blood
 CC coagulation and also for reducing TF levels in a mammal. The antibodies
 CC can be used, e.g. to treat thromboses, particularly to prevent or
 CC inhibit restenosis, or other thromboses following an invasive medical
 CC procedure such as arterial or cardiac surgery (e.g. angioplasty,
 CC endarterectomy, deployment of a stent, use of catheter, graft
 CC implantation or use of an arteriovenous shunt). The antibodies can also
 CC be used as a carrier for drugs, particularly pharmaceuticals targeted
 CC for interaction with a blood clot such as streptokinase, tissue
 CC plasminogen activator (t-PA) or urokinase, or a cytotoxic agent by
 CC conjugating a suitable toxin to the antibody. Further the antibodies
 CC can be used for treating a thromboembolic condition associated with
 CC cardiovascular disease, an infectious disease, a neoplastic disease or
 CC as a thrombolytic agent. The antibodies can also be used for detection
 CC and diagnosis.
 XX
 XX Sequence 117 AA;

Query Match 95.8%; Score 91; DB 19; Length 117;
 Best Local Similarity 94.1%; Pred. No. 3.5e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITIYDQNLKG 17
 |||||
 DB 50 YIDPYNGITIYDQNFKG 66

RESULT 3
 AAY52755 standard; Protein; 118 AA.
 ID AAY52755
 XX
 AC AAY52755;
 DT 26-JAN-2000 (first entry)
 XX
 DE Anti-tissue factor mouse monoclonal antibody ATR-2 H chain V region.
 XX
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX WO9951743-A1.
 PN
 XX 14-OCT-1999.
 PD
 XX
 XX 02-APR-1999; 99WO-JF01768.
 PF
 XX
 XX 03-APR-1998; 98JP-0091850.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Sato K, Adachi H, Yabuta N;
 PI WPI; 1999-620204/53.
 DR N-PSDB; AAZ33006.
 DR
 XX Humanised antibody recognizing human tissue factor, used for treatment
 PT of disseminated intravascular coagulation -
 PT
 PS Claim 1; Page 274; 291pp; Japanese.

CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrf) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)

CC chains containing the variable region of the L chain of a mouse
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has
 CC the high hTF binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 CC AA52767 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 118 AA;
 SQ Query Match 75.8%; Score 72; DB 20; Length 118;
 Best Local Similarity 76.5%; Pred. No. 0.00048;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
 DB 50 YIDPYNGGTYNQKFKG 66
 ||||| |||: ||
 ||||| |||: ||

RESULT 4
 AA52756
 ID AA52756 standard; Protein; 118 AA.

XX AC AA52756;
 XX DT 26-JAN-2000 (first entry)

XX DE Anti-tissue factor mouse monoclonal antibody ATR-3 H chain V region.

XX KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.

XX OS Synthetic.
 OS Mus sp.

XX PN WO9951743-A1.

XX PD 14-OCT-1999.

XX PF 02-APR-1999; 99WO-JP01768.

XX PR 03-APR-1998; 98JP-0091850.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Sato K, Adachi H, Yabuta N;

XX DR WPI; 1999-620204/53.

XX DR N-PSDB; AA233007.

XX PT Humanised antibody recognising human tissue factor, used for treatment
 PT of disseminated intravascular coagulation -

XX PS Claim 1; Page 275; 291pp; Japanese.

XX CC The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hTF) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
 CC chains containing the variable region of the L chain of a mouse
 CC monoclonal Ab recognising human tissue factor (hTF) and the constant
 CC region of the L chain of a human Ab, the variable region being one of six
 CC specified sequences (which are the L chain variable regions from mouse
 CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
 CC the treatment and prevention of thrombotic disease, especially of
 CC disseminated intravascular coagulation (DIC). The humanised antibody has

CC the high hTF binding activity of the mouse monoclonal antibody but
 CC greatly reduced immunogenicity. AA233001 to AA233091 and Y527007 to
 CC AA52767 represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 118 AA;

XX Query Match 75.8%; Score 72; DB 20; Length 118;
 XX Best Local Similarity 76.5%; Pred. No. 0.00048;
 XX Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
 DB 50 YIDPYNGGTYNQKFKG 66
 ||||| |||: ||
 ||||| |||: ||

RESULT 5
 AA52756
 ID AA52756 standard; Protein; 110 AA.

XX AC AA52756;

XX DT 15-MAR-1999 (first entry)

XX DE Vitronectin alpha-v beta-3 MAB VH.

XX KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.

XX OS Mus sp.

XX PN WO9840488-A1.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US04987.

XX PR 12-MAR-1997; 97US-0039609.

XX PA (SMIX) SMITHKLINE BEECHAM CORP.

XX PI Johanson KO, Jonak ZL, Taylor AH;

XX DR WPI; 1999-034590/03.

XX DR N-PSDB; AA71801.

XX PT New anti alpha-v beta-3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis

XX PS Example 13; Page 63; 97pp; English.

XX CC This is the amino acid sequence of the region of the murine
 CC monoclonal antibody (MAB) D12 heavy chain variable region (VH)
 CC that is altered in humanised D12 VH (see also AA584097). A
 CC synthetic gene (see AA581901) encoding the protein was prepared
 CC from synthetic oligonucleotides and used to prepare an expression
 CC vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3
 CC vitronectin receptor MAB. Humanised D12 MABs can be used for
 CC passive immunotherapy of disorders mediated by the alpha-v beta-3
 CC vitronectin receptor, e.g. restenosis and angiogenic associated
 CC diseases.

XX Sequence 110 AA;

XX Query Match 72.6%; Score 69; DB 20; Length 110;
 XX Best Local Similarity 70.6%; Pred. No. 0.0014;
 XX Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

CC of malignancy, osteolytic lesions produced by bone metastasis, bone
CC loss due to immobilisation or sex hormone deficiency. They can also
CC be used for targeted drug therapy, and for detection and diagnosis.

XX
SQ Sequence 117 AA;

Query Match 72.6%; Score 69; DB 20; Length 117;
Best Local Similarity 70.6%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
| | | | | | | | | | | | | | | | | | | |
Db 50 YIDPYNGDTFYNQKFG 66

RESULT 7
AAW84097
ID AAW84097 standard; Protein; 117 AA.
XX
AC AAW84097;
XX
DT 15-MAR-1999 (first entry)
XX
DE Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VH.
XX
KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12HZHC-10.
XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Region 31..35 /label= CDR1
FT Region 50..66 /label= CDR2
FT Region 99..106 /label= CDR3

XX
PN WO9840488-A1.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04987.
XX
PR 12-MAR-1997; 97US-0039609.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Johanson KO, Jonak ZL, Taylor AH;
XX
DR WPI; 1999-034590/03.
DR N-PSDB; AAV71799.

XX
New anti alpha v beta 3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

XX
PS Example 13; Page 56; 97pp; English.

XX
CC This is the amino acid sequence of the heavy chain variable region
CC (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine
CC monoclonal antibody D12, as deduced from isolated cDNA (see
CC AAV71797). D12 VH and VL (see AAW84094) show sequence similarity
CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
CC AAW84098) were constructed by combining the framework regions of the
CC human V region consensus sequences with complementarity determining
CC regions of D12 (keeping some preferred murine framework residues).
CC The humanised antibodies are specifically reactive with the human
CC alpha-v beta-3 protein receptor and capable of neutralising the
CC receptor. They can be used for passive immunotherapy of a disorder
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC disorders or angiogenic-related disorders, such as angiogenesis
CC restenosis, chronic inflammatory disorders, macular degeneration,
CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC diseases where bone resorption is associated with pathology such as
CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia

QY 1 YIDPYNGITTYDQNLKG 17
| | | | | | | | | | | | | | | | | | | |
Db 48 YIDPYNGDTFYNQKFG 64

RESULT 6
AAW84093
ID AAW84093 standard; Protein; 117 AA.
XX
AC AAW84093;
XX
DT 15-MAR-1999 (first entry)
XX
DE Murine vitronectin alpha-v beta-3 receptor MAb VH region.
XX
KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
XX
OS Mus sp.

XX
FH Key Location/Qualifiers
FT Region 31..35 /label= CDR1
FT Region 50..66 /label= CDR2
FT Region 99..106 /label= CDR3

XX
PN WO9840488-A1.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US04987.
XX
PR 12-MAR-1997; 97US-0039609.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Johanson KO, Jonak ZL, Taylor AH;
XX
DR WPI; 1999-034590/03.
XX
New anti alpha v beta 3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

XX
PS Example 13; Page 56; 97pp; English.

XX
CC This is the amino acid sequence of the heavy chain variable region
CC (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine
CC monoclonal antibody D12, as deduced from isolated cDNA (see
CC AAV71797). D12 VH and VL (see AAW84094) show sequence similarity
CC to Kabat VH subgroup I (see AAW84095) and Kabat VK subgroup III (see
CC AAW84096), respectively. Humanised VH (see AAW84097) and VL (see
CC AAW84098) were constructed by combining the framework regions of the
CC human V region consensus sequences with complementarity determining
CC regions of D12 (keeping some preferred murine framework residues).
CC The humanised antibodies are specifically reactive with the human
CC alpha-v beta-3 protein receptor and capable of neutralising the
CC receptor. They can be used for passive immunotherapy of a disorder
CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC disorders or angiogenic-related disorders, such as angiogenesis
CC restenosis, chronic inflammatory disorders, macular degeneration,
CC rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC diseases where bone resorption is associated with pathology such as
CC osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia

CC are retained. The humanised heavy chain can be expressed in host
 CC cells using nucleic acid molecules (see AAV71799) of the invention.
 CC Humanised D12 VL is also provided (see AAW84098)). The humanised
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
 CC angiogenic-related disorders, such as angiogenesis associated
 CC with diabetic retinopathy, atherosclerosis and restenosis, chronic
 CC inflammatory disorders, macular degeneration, rheumatoid arthritis
 CC and cancer, e.g. solid tumour metastasis, and diseases where bone
 CC resorption is associated with pathology such as osteoporosis,
 CC hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
 CC osteolytic lesions produced by bone metastasis, bone loss due to
 CC immobilisation or sex hormone deficiency. They can also be used for
 CC targeted drug therapy, and for detection and diagnosis.

XX SQ Sequence 117 AA;
 Query Match 72.6%; Score 69; DB 20; Length 117;
 Best Local Similarity 70.6%; Pred. No. 0.0015;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITFYDQNLKG 17
 |||||
 Db 50 YIDPYNGDTFYNQKPKG 66

RESULT 8
 AAW22418
 ID AAW22418 standard; Protein; 116 AA.

XX AC AAW22418;

DT 08-DEC-1997 (first entry)

XX DE Reshaped human AUK12-20 VH.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
 KW transplant rejection; graft versus host disease; nephritis;
 KW atopic dermatitis; psoriasis; myocardial ischaemia;
 XX acute leukocyte mediated lung injury; therapy; AUK12-20.

XX Chimeric Homo sapiens;
 OS Chimeric synthetic.

Key	Location/Qualifiers
FT Region	1..30
FT	/label= FR1
FT Region	31..35
FT	/label= CDR1
FT Region	36..49
FT	/label= FR2
FT Region	50..66
FT	/label= CDR2
FT Region	67..98
FT	/label= FR3
FT Region	99..105
FT	/label= CDR3
FT Region	106..116
FT	/label= FR4

XX WO9718838-A1.

XX 29-MAY-1997.

XX 21-NOV-1996; 96WO-US18807.

XX 21-NOV-1995; 95US-0561521.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MW, Jones ST, Leger OJ, Saldanha J, Yednock TA;

XX WPI; 1997-297879/27.
 DR Uses of humanised alpha-4 integrin antibody - for treatment of
 PT asthma, atherosclerosis, AIDS, dementia, etc.
 XX Example 6; Page 44; 107pp; English.

XX This polypeptide comprises version 'b', of a reshaped human
 CC antibody AUK12-20 VH region. A DNA fragment encoding the
 CC polypeptide was subcloned into vector pUC19 for use as a template
 CC for PCR amplification and production of version 'a' of a reshaped
 CC human 21.6 VH region (see AAW22413) that can be used in the
 CC construction of novel humanised anti-alpha-4 integrin antibodies.
 CC Claimed humanised antibodies are useful in the treatment of
 CC asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
 CC bowel disease, rheumatoid arthritis, transplant rejection, graft
 CC versus host disease, tumour metastasis, nephritis, atopic
 CC dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
 CC mediated lung injury.

XX SQ Sequence 116 AA;

Query Match 65.3%; Score 62; DB 18; Length 116;
 Best Local Similarity 64.7%; Pred. No. 0.021;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITFYDQNLKG 17
 |||||
 Db 50 YIDPFNGGTYSNQKPKG 66

RESULT 9

AAW29016

ID AAW29016 standard; Protein; 135 AA.

XX AC AAW29016;

XX 25-MAR-2003 (updated)

DT 30-MAR-1993 (first entry)

XX pUC-RVh-1220b.

XX Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
 KW complementarity determining region; monoclonal; hybridoma; PCR;
 KW plasmid; polymerase chain reaction; amplify.

XX Synthetic.

Key	Location/Qualifiers
FT Peptide	1..19
FT	/note= "Leader peptide"
FT Region	20..49
FT	/label= FR1
FT Region	50..54
FT	/label= CDR1
FT Region	55..68
FT	/label= FR2
FT Region	69..85
FT	/label= CDR2
FT Region	86..117
FT	/label= FR3
FT Region	118..124
FT	/label= CDR3
FT Region	125..135
FT	/label= FR4

XX WO9219759-A1.

XX 12-NOV-1992.

XX 24-APR-1992; 92WO-JP00544.

XX

XX (CHUS) CHUGAI SEIYAKU KK.
 XX Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 XX WPI; 1992-398882/48.
 XX N-PSDB; AAC30754.
 XX Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 XX Disclosure; Page 119-20; 207pp; Japanese.
 XX The sequences given in AAR28668-69 were encoded by plasmid sequences
 CC which were used in example to illustrate the production of a human
 CC antibody which recognises human interleukin-6 receptor (IL-6R). The
 CC antibody comprises light (L) chain and heavy (H) chain variable
 CC regions which were derived from a mouse monoclonal antibody produced
 CC from the hybridoma AUK12-20 which contained the plasmids p12-K2 and
 CC p12-h2.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 135 AA;
 Query Match 65.3%; Score 62; DB 13; Length 135;
 Best Local Similarity 64.7%; Pred. No. 0.025;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YIDPYNGITTYDQNLKG 17
 DB 69 YIDPFGGTSYNQKFKG 85
 RESULT 12
 ABP96759
 ID ABP96759 standard; Protein; 214 AA.
 AC ABP96759;
 XX 05-JUN-2003 (first entry)
 DT TSH receptor antibody 17D2 heavy chain amino acid sequence.
 DE Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 XX Synthetic.
 OS WO2003018632-A2.
 PN 06-MAR-2003.
 PD 21-AUG-2002; 2002WO-GB03831.
 XX 23-AUG-2001; 2001GB-0020649.
 XX 01-JUL-2002; 2002GB-0015212.
 XX (RSRR-) RSR LTD.
 PA Smith BR, Furmaniak J, Sanders JF;
 XX WPI; 2003-290051/28.
 XX N-PSDB; ACC44914.
 XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating
 PT an autoimmune disease associated with an immune reaction to a TSH
 PT receptor, e.g. thyroid cancer -
 XX Claim 71; Fig 17; 196pp; English.
 PS
 XX

CC The present invention describes a polypeptide sequence comprising part
 CC or all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of
 CC binding to a TSH receptor to stimulate the TSH receptor, where the
 CC binding partner does not comprise TSH or naturally produced antibodies to
 CC the TSH receptor; and (4) a combination comprising the binding partner
 CC and one or more further agents capable of stimulating thyroid tissue,
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid cancer.
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention.
 XX SQ Sequence 214 AA;
 Query Match 65.3%; Score 62; DB 24; Length 214;
 Best Local Similarity 64.7%; Pred. No. 0.044;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 YIDPYNGITTYDQNLKG 17
 DB 50 YIDPYSGATSYHQKFKG 66
 RESULT 13
 ABP96760
 ID ABP96760 standard; Protein; 214 AA.
 AC ABP96760;
 XX 05-JUN-2003 (first entry)
 DT TSH receptor antibody 17D2 heavy chain amino acid sequence.
 DE Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 XX Synthetic.
 OS WO2003018632-A2.
 PN 06-MAR-2003.
 PD 21-AUG-2002; 2002WO-GB03831.
 XX 23-AUG-2001; 2001GB-0020649.
 XX 01-JUL-2002; 2002GB-0015212.
 XX (RSRR-) RSR LTD.
 PA Smith BR, Furmaniak J, Sanders JF;
 XX WPI; 2003-290051/28.
 XX N-PSDB; ACC44915.
 XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating

PT an autoimmune disease associated with an immune reaction to a TSH
 XX receptor, e.g. thyroid cancer -
 XX
 PS Claim 67; Fig 18; 196pp; English.
 XX
 CC The present invention describes a polypeptide sequence comprising part
 CC or all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of
 CC binding to a TSH receptor to stimulate the TSH receptor, where the
 CC binding partner does not comprise TSH or naturally produced antibodies to
 CC the TSH receptor; and (4) a combination comprising the binding partner
 CC and one or more further agents capable of stimulating thyroid tissue,
 CC and/or tissue containing a TSH receptor, for simultaneous, separate or
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid tissue
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 214 AA;

Query Match 65.3%; Score 62; DB 24; Length 214;
 Best Local Similarity 64.7%; Pred. No. 0.044;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YIDPYNGITIDONLKG 17
 |||||:|:|:|:|:
 Db 50 YIDPYSGATYHQKFKG 66

RESULT 14
 AAR34670
 ID AAR34670 standard; Protein; 119 AA.
 XX
 AC AAR34670;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-AUG-1993 (first entry)
 XX
 DE VH Fv fragment of antidigitoxin monoclonal antibody 26-10.
 XX
 KW Heavy; light; variable; VH; VL; region; antidigitoxin; monoclonal;
 KW antibody; Mab; 26-10; Fv; fragment; antigen; binding site; linker;
 KW expression-secretion system; T7 promoter; signal peptide; molecule;
 KW polymerase chain reaction; PCR; single chain.
 XX
 OS Synthetic.
 XX
 PN WO9308300-A1.
 XX
 PD 29-APR-1993.
 XX
 PF 16-OCT-1992; 92WO-US08881.
 XX
 PR 18-OCT-1991; 91US-0777709.
 XX
 PA (UYCA-) UNIV CALGARY.
 XX
 PI Anthony JG, Ng SC, Wong S;

XX
 DR WPI; 1993-152491/18.
 DR N-PSDB; AAQ41065.
 XX
 PT Expression-secretion vectors - for prodn. of biologically active
 PT antibody Fv fragments or single chain Fv molecules
 PS
 PS Disclosure; Fig 1A; 51pp; English.

XX The sequences given in AAR34670-71 represent the heavy and light
 CC variable portions (VH and VL) of antidigitoxin monoclonal antibody (Mab)
 CC 26-10. These VH and VL peptide fragments are examples of Fv fragments.
 CC Fv fragments are the smallest complete antigen binding sites presently
 CC known. The DNA fragments encoding these Fv fragments were used in the
 CC construction of an expression-secretion system for the production
 CC of biologically active Fv fragments. The system also contains a DNA
 CC sequence encoding the T7 promoter and one or DNA sequences encoding
 CC one or more signal peptides (see also AAR38527-28). The secretion-
 CC expression vector was produced by polymerase chain reaction. Fv
 CC fragments may also be produced as single chain Fv molecules (see
 CC also AAR34672) which contain the VH and VL regions, a signal sequence
 CC and a linker between the two variable regions. Fv fragments and
 CC single chain molecules may be used to specifically bind one or more
 CC of the same antigens as the full length antibody from which it is
 CC derived.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 119 AA;

Query Match 63.2%; Score 60; DB 14; Length 119;
 Best Local Similarity 58.8%; Pred. No. 0.046;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIDONLKG 17
 |||||:|:|:|:|:
 Db 50 YISPSGVGTGYNQKFKG 66

RESULT 15
 AAR38586
 ID AAR38586 standard; Protein; 119 AA.
 XX
 AC AAR38586;
 XX
 DT 25-MAR-2003 (updated)
 DT 28-JUL-1995 (first entry)
 XX
 DE Antidigitoxin monoclonal antibody 26-10 heavy chain variable region.
 XX
 KW Single chain antibody Fv fragment; monoclonal antibody 26-10;
 KW anti-digoxin; scFv; heavy chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN WO9312246-A1.
 XX
 PD 24-JUN-1993.
 XX
 PF 18-DEC-1991; 91WO-US07625.
 XX
 PR 18-DEC-1991; 91WO-US07625.
 PR 18-DEC-1991; 91EP-0923150.
 XX
 PA (ANTH/) ANTHONY J G.
 PA (NGSC/) NG S C.
 PA (UYCA-) UNIV CALGARY.
 PA (WONG/) WONG S.
 XX
 PI Anthony JG, Ng S, Wong S, Ng SC;

XX
 DR WPI; 1993-214187/26.
 DR N-PSDB; AAQ44036.
 XX

PT Expression-secretion vectors for prodn. of Fv fragments - used
PT for similar applications as whole antibodies and specifically
PT bind digoxin
XX
XX
PS Claim 13; Fig 1A; 55pp; English.
XX
CC Antidigoxin monoclonal antibody 26-10 is a high affinity antibody
CC produced against digoxin conjugated to BSA. cDNA clones of the genes
CC encoding the VH and VL portions of the 26-10 antibody were made by
CC PCR amplification of cDNA generated by reverse transcription of mRNA
CC isolated from 2610 hybridoma. The VH and VL clones (encoding AAR38586
CC and AAR38587, respectively) were used in the construction of plasmids
CC for the expression of single-chain Fv fragments.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ

Sequence 119 AA;
Query Match 63.2%; Score 60; DB 14; Length 119;
Best Local Similarity 58.8%; Pred. No. 0.046;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITIVDQNLKG 17
|||:|:|:|:
Db 50 YISPTSGVTGYNQKFKG 66

Search completed: January 13, 2004, 12:38:29
Job time : 3.96419 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2004, 12:43:20 ; Search time 2.71703 Seconds

(without alignments)
1260.812 Million cell updates/sec

Title: US-09-990-586-101

Perfect score: 95

Sequence: 1 YIDPYNGITTYDQNLKG 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	17	11	US-09-990-586-101
2	95	100.0	17	12	Sequence 101, App
3	95	100.0	17	12	Sequence 164, App
4	91	95.8	17	10	US-10-230-880-101
5	91	95.8	17	10	Sequence 101, App
6	91	95.8	17	12	US-09-293-854-9
7	91	95.8	17	12	Sequence 9, Appli
8	91	95.8	17	12	US-09-990-586-9
9	91	95.8	17	12	Sequence 9, Appli
10	91	95.8	17	12	US-10-310-113-9
11	91	95.8	17	12	Sequence 161, App
12	91	95.8	17	12	US-10-230-880-9
13	91	95.8	17	12	Sequence 9, Appli
14	91	95.8	17	15	US-10-293-417-9
15	91	95.8	17	15	Sequence 9, Appli
16	91	95.8	117	11	US-09-293-854-4
17	91	95.8	117	11	Sequence 4, Appli
18	91	95.8	117	11	US-09-990-586-4
19	91	95.8	117	12	Sequence 4, Appli
20	91	95.8	117	12	US-10-310-113-4
21	91	95.8	117	12	Sequence 4, Appli
22	91	95.8	117	12	US-10-230-880-4
23	91	95.8	117	15	Sequence 4, Appli
24	91	95.8	117	15	US-10-293-417-4
25	69	72.6	110	12	US-10-223-880-12

16	69	72.6	117	12	US-10-223-880-2	Sequence 2, Appli
17	69	72.6	117	12	US-10-223-880-5	Sequence 5, Appli
18	60	63.2	252	10	US-08-887-853-4	Sequence 4, Appli
19	60	63.2	260	11	US-08-887-853-2	Sequence 2, Appli
20	60	63.2	260	11	US-08-782-672-2	Sequence 2, Appli
21	59	62.1	117	11	US-09-782-672B-2	Sequence 48, Appli
22	59	62.1	117	11	US-09-726-258-48	Sequence 49, Appli
23	59	62.1	117	11	US-09-726-258-49	Sequence 37, Appli
24	59	62.1	135	11	US-09-726-258-37	Sequence 44, Appli
25	59	62.1	253	11	US-09-726-258-44	Sequence 52, Appli
26	59	62.1	253	11	US-09-726-258-52	Sequence 55, Appli
27	59	62.1	253	11	US-09-726-258-55	Sequence 70, Appli
28	59	62.1	256	11	US-09-726-258-70	Sequence 60, Appli
29	59	62.1	298	11	US-09-726-258-60	Sequence 60, Appli
30	59	62.1	452	11	US-09-726-258-71	Sequence 71, Appli
31	57	60.0	116	11	US-09-940-727B-62	Sequence 62, Appli
32	57	60.0	116	11	US-09-940-727B-15	Sequence 15, Appli
33	57	60.0	116	11	US-09-940-727B-90	Sequence 90, Appli
34	57	60.0	127	10	US-08-998-831-7	Sequence 7, Appli
35	57	60.0	127	12	US-10-373-561-7	Sequence 65, Appli
36	56	58.9	17	11	US-09-940-727B-65	Sequence 12, Appli
37	55	57.9	110	11	US-09-940-727B-86	Sequence 86, Appli
38	55	57.9	17	14	US-10-032-482-12	Sequence 12, Appli
39	55	57.9	20	14	US-10-032-482-23	Sequence 23, Appli
40	55	57.9	106	14	US-10-032-482-3	Sequence 3, Appli
41	55	57.9	274	9	US-09-813-659-30	Sequence 30, Appli
42	55	57.9	274	12	US-10-283-610A-30	Sequence 30, Appli
43	55	57.9	302	9	US-09-813-659-32	Sequence 32, Appli
44	55	57.9	302	12	US-10-283-610A-32	Sequence 32, Appli
45	54	56.8	504	15	US-10-207-655-348	Sequence 348, App
			119	12	US-10-389-155-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1

US-09-990-586-101
; Sequence 101, Application US/09990586
; Publication No. US20030109680A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, HING C.
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SEQ ID NO 101
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-101

Query Match 100.0%; Score 95; DB 11; Length 17;

Best Local Similarity 100.0%; Pred. No. 5,5e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPYNGITTYDQNLKG 17

RESULT 2

US-10-310-113-164
; Sequence 164, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, HING C.
; APPLICANT: WONG, HING C.

APPLICANT: NIEVES, ESPERANZA LILIANA
APPLICANT: MOSQUERA, LUIS A.
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: THROMBOSES
FILE REFERENCE: 58122(71758)
CURRENT APPLICATION NUMBER: US/10/310,113
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 08/814,806
PRIOR FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 164
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: humanized HC-08 CDR2 amino acid sequence
US-10-310-113-164

Query Match 100.0%; Score 95; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIDPYNGITIIDQNLKG 17
Db 1 YIDPYNGITIIDQNLKG 17

RESULT 3
US-10-230-880-101
Sequence 101, Application US/10230880
Publication No. US20030190705A1
GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71758/58066
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 101
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-230-880-101

Query Match 100.0%; Score 95; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YIDPYNGITIIDQNLKG 17
Db 1 YIDPYNGITIIDQNLKG 17

RESULT 4
US-09-293-854-9
Sequence 9, Application US/09293854

Patent No. US20020168357A1
GENERAL INFORMATION:
APPLICANT: WONG, HING C.
Jiao, Jin-an
Esperanza, Nieves
Lawrence, Lupehschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/814,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CORLESS, PETER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-293-854-9

Query Match 95.8%; Score 91; DB 10; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITIIDQNLKG 17
Db 1 YIDPYNGITIIDQNLKG 17

RESULT 5
US-09-990-586-9
Sequence 9, Application US/0990586
Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16

STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/293,417
FILING DATE: 12-Nov-99 US20030082636A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
APPLICATION NUMBER: 08/814,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-293-417-9
Query Match 95.8%; Score 91; DB 15; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPYNGITTYDQNLKG 17
RESULT 10
US-09-293-854-4
Sequence 4, Application US/09293854
Patent No. US20020168357A1
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
Jiao, Jin-an
Eperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/814,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4
Query Match 95.8%; Score 91; DB 10; Length 117;
Best Local Similarity 94.1%; Pred. No. 2.2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPYNGITTYDQNLKG 66
RESULT 11
US-09-990-586-4
Sequence 4, Application US/09990586
Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-990-586-4
Query Match 95.8%; Score 91; DB 11; Length 117;
Best Local Similarity 94.1%; Pred. No. 2.2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPYNGITTYDQNLKG 66
RESULT 12
US-10-310-113-4
Sequence 4, Application US/10310113
Publication No. US20030176664A1
GENERAL INFORMATION:

APPLICANT: JIAO, JIN-AN
 APPLICANT: WONG, HING C.
 APPLICANT: NIEVES, ESPERANZA LILIANA
 APPLICANT: MOSQUERA, LUIS A.
 TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
 TITLE OF INVENTION: THROMBOSES
 FILE REFERENCE: 58122(71758)
 CURRENT APPLICATION NUMBER: US/10/310,113
 PRIOR FILING DATE: 2002-12-04
 PRIOR APPLICATION NUMBER: 09/990,586
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: 60/343,306
 PRIOR FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: 09/293,854
 PRIOR FILING DATE: 1999-04-16
 PRIOR APPLICATION NUMBER: 08/814,806
 PRIOR FILING DATE: 1997-03-10
 NUMBER OF SEQ ID NOS: 169
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 4
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Murine sp.
 US-10-310-113-4

Query Match 95.8%; Score 91; DB 12; Length 117;
 Best Local Similarity 94.1%; Pred. No. 2.2e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNIGITIDQNLKG 17
 DB 50 YIDPYNIGITIDQNFKG 66

RESULT 13
 US-10-230-880-4
 Sequence 4, Application US/10230880
 Publication No. US20030190705A1
 GENERAL INFORMATION:
 APPLICANT: WONG, HING C.
 APPLICANT: STINSON, JEFFREY L.
 APPLICANT: MOSQUERA, LUIS A.
 TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
 FILE REFERENCE: 71758/58066
 CURRENT APPLICATION NUMBER: US/10/230,880
 CURRENT FILING DATE: 2002-12-23
 PRIOR APPLICATION NUMBER: 09/990,586
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: 60/343,306
 PRIOR FILING DATE: 2001-10-29
 PRIOR APPLICATION NUMBER: 09/293,854
 PRIOR FILING DATE: 1999-04-16
 NUMBER OF SEQ ID NOS: 174
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 4
 LENGTH: 117
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-230-880-4

Query Match 95.8%; Score 91; DB 12; Length 117;
 Best Local Similarity 94.1%; Pred. No. 2.2e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNIGITIDQNLKG 17
 DB 50 YIDPYNIGITIDQNFKG 66

RESULT 14
 US-10-293-417-4
 Sequence 4, Application US/10293417
 Publication No. US20030082636A1

GENERAL INFORMATION:
 APPLICANT: Wong, Hing C.
 APPLICANT: Jiao, Jin-an
 APPLICANT: Esperanza, Nieves
 APPLICANT: Lawrence, Luessenchen
 TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
 COAGULATION AND METHODS OF USE THEREOF
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSES: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM COMPATIBLE
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ VERSION 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/293,417
 FILING DATE: 12-NO. US20030082636A1-2002
 CLASSIFICATION: <UNKNOWN>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/293,854
 FILING DATE: 16-APR-1999
 APPLICATION NUMBER: 08/814,806
 FILING DATE: <UNKNOWN>
 ATTORNEY/AGENT INFORMATION:
 NAME: CORLESS, PETER F.
 REGISTRATION NUMBER: 33,860
 REFERENCE/DOCKET NUMBER: 46943
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 TELEX: <UNKNOWN>
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-293-417-4

Query Match 95.8%; Score 91; DB 15; Length 117;
 Best Local Similarity 94.1%; Pred. No. 2.2e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNIGITIDQNLKG 17
 DB 50 YIDPYNIGITIDQNFKG 66

RESULT 15
 US-10-223-880-12
 Sequence 12, Application US/10223880
 Publication No. US20030152571A1
 GENERAL INFORMATION:
 APPLICANT: JONAK, ZDENKA
 APPLICANT: JOHANSON, KYUNG O.
 APPLICANT: TAYLOR, ALEXANDER
 TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL
 ANTIBODIES
 FILE REFERENCE: P50629C1
 CURRENT APPLICATION NUMBER: US/10/223,880
 CURRENT FILING DATE: 2002-08-20

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; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-223-880-12
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Query Match      72.6%; Score 69; DB 12; Length 110;
Best Local Similarity 70.6%; Pred.No. 0.00085;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 YIDPYNGITIYDQNLKG 17
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DB      48 YIDPYNGDTFYNQKFKG 64
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Search completed: January 13, 2004, 13:13:47
Job time : 2.71703 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 13, 2004, 12:33:50 ; Search time 1.46987 Seconds
(without alignments)
489.353 Million cell updates/sec

Title: US-09-990-586-101
Perfect score: 95
Sequence: 1 VIDPYNGITTYDQNLKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	95.8	17	2	US-08-814-806-9
2	91	95.8	17	4	US-09-293-854-9
3	91	95.8	117	2	US-08-814-806-4
4	91	95.8	117	4	US-09-293-854-4
5	62	65.3	17	1	US-08-137-117D-144
6	62	65.3	17	2	US-08-436-717-144
7	62	65.3	116	2	US-08-561-521-41
8	62	65.3	116	5	PCT-US95-01219-41
9	62	65.3	135	1	US-08-137-117D-27
10	62	65.3	135	1	US-08-137-117D-100
11	62	65.3	135	1	US-08-137-117D-102
12	62	65.3	135	1	US-08-137-117D-112
13	62	65.3	135	2	US-08-436-717-27
14	62	65.3	135	2	US-08-436-717-100
15	62	65.3	135	2	US-08-436-717-102
16	62	65.3	135	2	US-08-436-717-112
17	60	63.2	246	1	US-08-257-341-7
18	60	63.2	252	1	US-08-133-804-4
19	60	63.2	252	1	US-08-461-838-4
20	60	63.2	252	1	US-08-461-386-4
21	60	63.2	260	2	US-08-447-402-1
22	60	63.2	269	3	US-09-070-408-132
23	60	63.2	367	1	US-08-257-341-5
24	59	62.1	117	3	US-09-027-449-48
25	59	62.1	117	3	US-09-027-449-49
26	59	62.1	117	3	US-08-804-444A-48
27	59	62.1	117	3	US-08-804-444A-49

28	59	62.1	117	3	US-09-026-985-48	Sequence 48, Appl
29	59	62.1	117	3	US-09-026-985-49	Sequence 49, Appl
30	59	62.1	117	4	US-09-121-952A-48	Sequence 48, Appl
31	59	62.1	117	4	US-09-121-952A-49	Sequence 49, Appl
32	59	62.1	117	4	US-09-234-340A-48	Sequence 48, Appl
33	59	62.1	117	4	US-09-234-340A-49	Sequence 49, Appl
34	59	62.1	135	1	US-08-398-613A-50	Sequence 50, Appl
35	59	62.1	135	1	US-08-398-613A-50	Sequence 50, Appl
36	59	62.1	135	2	US-08-398-613A-50	Sequence 50, Appl
37	59	62.1	135	2	US-08-491-334A-50	Sequence 50, Appl
38	59	62.1	135	3	US-09-027-449-37	Sequence 37, Appl
39	59	62.1	135	3	US-08-804-444A-37	Sequence 37, Appl
40	59	62.1	135	3	US-09-026-985-37	Sequence 37, Appl
41	59	62.1	135	4	US-09-121-952A-37	Sequence 37, Appl
42	59	62.1	135	4	US-09-234-340A-37	Sequence 37, Appl
43	59	62.1	253	1	US-08-398-613A-58	Sequence 58, Appl
44	59	62.1	253	1	US-08-398-613A-58	Sequence 58, Appl
45	59	62.1	253	1	US-08-398-611A-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-08-814-806-9
; Sequence 9, Application US/08814806
; Patent No. 5986065
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; APPLICANT: Jiao, Jin-an
; APPLICANT: Esperanza, Nieves
; APPLICANT: Lawrence, Antiposchen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESS: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/814,806
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

Tue Jan 13 13:21:59 2004

US-08-814-806-9

Query Match 95.8%; Score 91; DB 2; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.5e-09;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPYNGITTYDQNLKG 17

RESULT 2

US-09-293-854-9
Sequence 9, Application US/09293854

Patent No. 655319

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.

Jiao, Jin-an

Esperanza, Nieves

Lawrence, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293,854

FILING DATE: 16-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/814,806

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Corless, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 46943

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-293-854-9

Query Match 95.8%; Score 91; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.5e-09;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPYNGITTYDQNLKG 17

RESULT 3

US-08-814-806-4

Sequence 4, Application US/08814806

Patent No. 596065

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.

Jiao, Jin-an

Esperanza, Nieves

Lawrence, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD

COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,806

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Corless, Peter F

REGISTRATION NUMBER: 33,860

REFERENCE/DOCKET NUMBER: 46943

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-814-806-4

Query Match 95.8%; Score 91; DB 2; Length 117;

Best Local Similarity 94.1%; Pred. No. 8.9e-08;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YIDPYNGITTYDQNLKG 17

Db 50 YIDPYNGITTYDQNLKG 66

RESULT 4

US-09-293-854-4

Sequence 4, Application US/09293854

Patent No. 655319

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.

Jiao, Jin-an

Esperanza, Nieves

Lawrence, Luepschen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD

COAGULATION AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 26

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;; STREET: 130 Water Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/293,854
;; FILING DATE: 16-Apr-1999
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/814,806
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Corless, Peter F
;; REGISTRATION NUMBER: 33,860
;; REFERENCE/DOCKET NUMBER: 46943
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-523-3400
;; TELEFAX: 617-523-6440
;; TELEX: <Unknown>
;;
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4

Query Match 95.8%; Score 91; DB 4; Length 117;
Best Local Similarity 94.1%; Pred. No. 8.9e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
|||:|||||:|||||
Db 50 YIDPYNGITTYDQNLKG 66

RESULT 5
US-08-137-117D-144
; Sequence 144, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/137,117D
;; FILING DATE: 20-DEC-1993
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/JP92/00544
;; FILING DATE: 24-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 4-32084
;; FILING DATE: 19-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 3-95476
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WEGNER, Harold C.
;; REGISTRATION NUMBER: 25,258
;; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 144:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-137-117D-144

Query Match 65.3%; Score 62; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.00053;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
|||:|||||:|||||
Db 1 YIDPFNGGTSYNQKFKG 17

RESULT 6
US-08-436-717-144
; Sequence 144, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
;

FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-144

Query Match 65.3%; Score 62; DB 2; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.00053;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPENGGSYNQKFKG 17

RESULT 7
US-08-561-521-41
Sequence 41, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-41

Query Match 65.3%; Score 62; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPENGGSYNQKFKG 66

RESULT 8
PCT-US95-01219-41
Sequence 41, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-41

Query Match 65.3%; Score 62; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPENGGSYNQKFKG 66

RESULT 9
US-08-137-117D-27
Sequence 27, Application US/08137117D

FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-436-717-144

Query Match 65.3%; Score 62; DB 2; Length 17;
Best Local Similarity 64.7%; Pred. No. 0.00053;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 1 YIDPENGGSYNQKFKG 17

RESULT 7
US-08-561-521-41
Sequence 41, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids

Query Match 65.3%; Score 62; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPENGGSYNQKFKG 66

RESULT 8
PCT-US95-01219-41
Sequence 41, Application PC/TUS9501219
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids

Query Match 65.3%; Score 62; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPYNGITTYDQNLKG 17
Db 50 YIDPENGGSYNQKFKG 66

RESULT 9
US-08-137-117D-27
Sequence 27, Application US/08137117D

Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SAITO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-27

Query Match 65.3%; Score 62; DB 1; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 4;

Qy 1 YIDPYNGITIDQNKLK 17
Db 69 YIDPFNGGTSYNQKFKG 85

RESULT 10
US-08-137-117D-100
Sequence 100, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SAITO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-100

Query Match 65.3%; Score 62; DB 1; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 4;

Qy 1 YIDPYNGITIDQNKLK 17
Db 69 YIDPFNGGTSYNQKFKG 85

RESULT 11
US-08-137-117D-102
Sequence 102, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SAITO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/137,117D
APPLICATION NUMBER: JP 4-32084
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-102

Query Match 65.3%; Score 62; DB 1; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPNGITIIYDQNLKG 17
||||:||||:||||
DB 69 YIDPFGGTSYNQKPKG 85

RESULT 12
US-08-137-117D-112
Sequence 112, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-137-117D-112

Query Match 65.3%; Score 62; DB 1; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YIDPNGITIIYDQNLKG 17
||||:||||:||||
DB 69 YIDPFGGTSYNQKPKG 85

RESULT 13
US-08-436-717-27
Sequence 27, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-27

Query Match 65.3%; Score 62; DB 2; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels 0;

QY 1 YIDPYNGITIVDQNLKG 17
|||:|||||:|
Db 69 YIDPFNGGTSYNQKFKG 85

RESULT 14

US-08-436-717-100
Sequence 100, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-100

Query Match 65.3%; Score 62; DB 2; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels 0;

QY 1 YIDPYNGITIVDQNLKG 17
|||:|||||:|
Db 69 YIDPFNGGTSYNQKFKG 85

RESULT 15

US-08-436-717-102
Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-717-102

Query Match 65.3%; Score 62; DB 2; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels 0;

Qy 1 YIDPVGITIIDONLKG 17
|||:|:|:|:|
Db 69 YIDPVGITSYNQKFG 85

Search completed: January 13, 2004, 12:46:36
Job time : 1.46987 secs